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OM protein - protein search, using sw model

Run on: December 3, 2002, 14:35:53 ; Search time 35 seconds
(without alignments)
612.953 Million cell updates/sec

Title: US-09-907-263-2
Perfect score: 941
Sequence: 1 DSVCPQKXHYHPQNNISCTT.....CSNCKKSLCTKLCFLQIEN 161
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues
Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq 101002.*
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22: /SID22/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	941	100.0	161	13	Native 30 kD TNF i
2	941	100.0	161	19	Human soluble tumo
3	941	100.0	161	19	Soluble tumour nec
4	941	100.0	161	20	Tumour necrosis in
5	941	100.0	161	22	Human 30 kDa TNF i
6	941	100.0	211	20	Tumour necrosis fa
7	941	100.0	280	22	Tnf1 protein. Un
8	941	100.0	309	16	TNF-R-GBPH fusion
9	941	100.0	311	20	Tumour necrosis fa
10	941	100.0	336	18	TBP(20-190)/hCG-be

11	941	100.0	366	20	AAW89228	Tumour necrosis fa
12	941	100.0	371	11	AAW07449	Tumour Necrosis Fa
13	941	100.0	397	20	AAW89227	Tumour necrosis fa
14	941	100.0	417	20	AAW89226	Tumour necrosis fa
15	941	100.0	420	20	AAW89224	Tumour necrosis fa
16	941	100.0	451	16	AAW70107	TNF-R-GBP 130 fusi
17	941	100.0	455	12	AAW10986	30kD TNF inhibitor
18	941	100.0	455	12	AAW11082	Human 55kD TNF-bin
19	941	100.0	455	13	AAW20787	TNF-alpha binding
20	941	100.0	455	13	AAW24000	TNF-alpha 55kD rec
21	941	100.0	455	14	AAW42059	Lambda derived TNF
22	941	100.0	455	16	AAW75084	p55 TNF-R. Homo s
23	941	100.0	455	20	AAW30934	Human tumour necro
24	941	100.0	455	21	AAW36266	Human tumour necro
25	941	100.0	455	21	AAW37800	Human tumour necro
26	941	100.0	455	21	AAW28984	Human TNFR 1. Hom
27	941	100.0	455	21	AAW23446	Human tumour necro
28	941	100.0	455	21	AAW01336	TNF-R1 death recep
29	941	100.0	455	22	AAW86817	Human TNFBP-associ
30	941	100.0	455	22	AAW36697	Human tumour necro
31	941	100.0	455	22	AAW37677	Human 30 kDa TNF i
32	941	100.0	455	23	AAW81649	Human tumour necro
33	941	100.0	455	23	AAW75064	Human tumour necro
34	941	100.0	455	23	AAW70104	TNF-R-GBPH fusion
35	941	100.0	884	16	AAW70109	TNF-R-GBP 130 fusi
36	941	100.0	900	16	AAW70103	TNF-R-GBP 130 fusi
37	941	100.0	1245	16	AAW70106	TNF-R-Pl. vivax Du
38	941	100.0	1604	16	AAW70105	TNF-R-EBA 175 fusi
39	938	99.7	455	11	AAW07451	Human Tumour Necro
40	932	99.0	433	14	AAW51032	Mutant p55 tumour
41	932	99.0	443	14	AAW51033	Mutant p55 tumour
42	932	99.0	455	14	AAW42197	p55 Tumour necrosi
43	932	99.0	455	14	AAW51034	Mutant p55 tumour
44	931	98.9	455	12	AAW12550	Type I TNF recepto
45	930.5	98.9	909	19	AAW64485	Human Fas protein.

ALIGNMENTS

RESULT 1
AAW27496
ID AAR27496 standard; protein; 161 AA.
XX AAR27496;
XX AC
XX DT 09-MAR-1993 (first entry)
XX DE Native 30 kD TNF inhibitor.
XX DE Tumour necrosis factor; ethylene glycol; pharmacokinetic;
XX KW adult respiratory distress syndrome; rheumatoid arthritis;
XX KW septic shock; pulmonary fibrosis; spacer.
XX OS Homo sapiens.
XX PN WO9216221-A.
XX PD 01-OCT-1992.
XX PF 13-MAR-1992; 92WO-US02122.
XX PR 15-MAR-1991; 91US-0659862.
XX PR 17-JAN-1992; 92US-0822296.
XX (SYND) SYNERGEN INC.
XX Armes LG, Brewer MT, Evans RJ, Kohno T, Thompson RC;
XX WPI; 1992-348933/42.
XX New ethylene glycolated polypeptide(s) with improved
XX pharmacokinetic properties - for treating e.g. TNF and IL-1

PT mediated diseases, e.g. adult respiratory distress syndrome,
PT rheumatoid arthritis, septic shock etc.

XX Claim 54; Fig 2; 100pp; English.

XX The sequence shows a native 30 kD TNF inhibitor which may be
CC modified to contain at least one non-native cysteine residue, pref.
CC at positions 1, 14, 105, 111 and/or 165. The non-native cysteine is
CC joined to a non-peptidic polymer, pref. monomethoxy PEG via
CC this non-peptidic spacer. Two such TNF inhibitor moieties may be linked via
CC this non-peptidic spacer. The modified polypeptides show improved
CC pharmacokinetic properties, i.e. increased mol. wt. hence reduced
CC clearance rate following s.c. or systemic administration, increased
CC sol. of native TNF inhibitors, and reduced antigenicity. The
CC polypeptides may be used for treatment of TNF mediated diseases such
CC as adult respiratory distress syndrome, pulmonary fibrosis, rheumatoid
CC arthritis, inflammatory bowel disease and septic shock. The same
CC method may be applied to the interleukin-1 receptor antagonist
CC IL-1ra. See also AAR27495.

XX Sequence 161 AA;

Query Match 100.0%; Score 941; DB 13; Length 161;
Best Local Similarity 100.0%; Pred. No. 2.4e-67;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSVCPQGYIHPNNSICTCKCHKGTLYLNDPCPGQDPTDCRECSGSFTASENHLRHCL 60
Db 1 DSVCPQGYIHPNNSICTCKCHKGTLYLNDPCPGQDPTDCRECSGSFTASENHLRHCL 60

Qy 61 SCSKCRKEMGVEIISCTVDRDVTGCGCRKNQYRHWSENLFQCFNCSCLNGTVHLSQOE 120
Db 61 SCSKCRKEMGVEIISCTVDRDVTGCGCRKNQYRHWSENLFQCFNCSCLNGTVHLSQOE 120

Qy 121 KONTVCTCHAGFFLENECVSCSNCKSLLECTKLCPLPIEN 161
Db 121 KONTVCTCHAGFFLENECVSCSNCKSLLECTKLCPLPIEN 161

RESULT 2

AAW59664 standard; Protein; 161 AA.

AAW59664;

28-SEP-1998 (first entry)

Human soluble tumour necrosis factor receptor type I.

Human; tumour necrosis factor; TNF; TNF receptor type I;
inflammatory disease; leukaemia; TNF binding protein;
anti-inflammatory drug; methotrexates.

Homo sapiens.

WO9824463-A2.

11-JUN-1998.

08-DEC-1997; 97WO-US22733.

09-JUL-1997; 97US-0052023.

06-DEC-1996; 96US-0032587.

23-JAN-1997; 97US-0036355.

07-FEB-1997; 97US-0039315.

(AMGE-) AMGEN INC.

Bendelet AM, Edwards CK, Sennello RM;

WPI; 1998-333039/29.
N-PSDB; AAV41548.

PT Treatment of acute or chronic inflammatory disease, e.g. leukaemia -
PT by administering tumour necrosis factor binding protein and at least
PT one additional anti-inflammatory drug, e.g. methotrexate

XX Disclosure; Fig 1; 104pp; English.

XX This is the amino acid sequence of the human tumour necrosis factor
CC receptor type I, used in the method of the invention involving the
CC treatment of acute or chronic inflammatory disease such as leukaemia
CC by administering tumour necrosis factor binding protein and at least
CC one additional anti-inflammatory drug, e.g. methotrexate.

XX Sequence 161 AA;

Query Match 100.0%; Score 941; DB 19; Length 161;
Best Local Similarity 100.0%; Pred. No. 2.4e-67;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSVCPQGYIHPNNSICTCKCHKGTLYLNDPCPGQDPTDCRECSGSFTASENHLRHCL 60
Db 1 DSVCPQGYIHPNNSICTCKCHKGTLYLNDPCPGQDPTDCRECSGSFTASENHLRHCL 60

Qy 61 SCSKCRKEMGVEIISCTVDRDVTGCGCRKNQYRHWSENLFQCFNCSCLNGTVHLSQOE 120
Db 61 SCSKCRKEMGVEIISCTVDRDVTGCGCRKNQYRHWSENLFQCFNCSCLNGTVHLSQOE 120

Qy 121 KONTVCTCHAGFFLENECVSCSNCKSLLECTKLCPLPIEN 161
Db 121 KONTVCTCHAGFFLENECVSCSNCKSLLECTKLCPLPIEN 161

RESULT 3

AAW52267 standard; Protein; 161 AA.

AAW52267;

29-JUN-1998 (first entry)

Soluble tumour necrosis factor receptor.

Soluble tumour necrosis factor receptor; sTNFR; TNF-mediated disease;
tumour necrosis factor binding protein; autoimmune disease; arthritis;
adult respiratory distress syndrome; cachexia/anorexia; cancer; therapy;
chronic fatigue syndrome; graft rejection; Alzheimer's disease; TNBP.

Homo sapiens.

WO9801555-A2.

15-JAN-1998.

09-JUL-1997; 97WO-US12244.

04-MAR-1997; 97US-0039792.

09-JUL-1996; 96US-0021443.

06-DEC-1996; 96US-0032534.

23-JAN-1997; 97US-0037737.

07-FEB-1997; 97US-0039314.

(AMGE-) AMGEN INC.

Edwards CK, Fisher EF, Kieft GL;

WPI; 1998-101052/09.

N-PSDB; AAV19801.

Truncated and soluble forms of tumour necrosis factor receptor -
PT useful for treating diseases involving factor, e.g. arthritis and
PT adult respiratory distress syndrome
XX Claim 1; Fig 1; 205pp; English.

This sequence is the human soluble tumour necrosis factor receptor (STNFR). The protein was used to make the truncated STNFR proteins of the invention. The truncated STNFR proteins and tumour necrosis factor binding proteins (TNBP) are used to treat any TNF-mediated disease, e.g. arthritis, adult respiratory distress syndrome, cachexia/anorexia, cancer, chronic fatigue syndrome, graft rejection, Alzheimer's disease and other autoimmune diseases. Cells transformed with a vector containing DNA encoding the protein may be used for production of recombinant STNFR, which may also be used for measuring the amount of STNFR in samples and to raise antibodies against STNFR. TNBP may also be used in preparation of therapeutic compositions for treating the above diseases. The STNFR proteins are well suited to large scale production (since they lack the dematation site in region 111-126, so are more stable in vivo); contain fewer disulphide bonds and fewer epitopes, making them less antigenic than full-length proteins.

Query Match 100.0%; Score 941; DB 19; Length 161;
Best Local Similarity 100.0%; Pred. No. 2.4e-67;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVCPQGYIHPQNNISICTCKHKGTYLYNDPCPGQDTCRECSGSFTASENHLRHCL 60
DB 1 DSVCPQGYIHPQNNISICTCKHKGTYLYNDPCPGQDTCRECSGSFTASENHLRHCL 60

QY 61 SCSKCRKEMGQVEISSCTVDRDTCGCRKNQYRHWSENLFQCFNCSLCNGTVHLSQOE 120
DB 61 SCSKCRKEMGQVEISSCTVDRDTCGCRKNQYRHWSENLFQCFNCSLCNGTVHLSQOE 120

QY 121 KQNTVCTCHAGFFLRENECVSCSNCKKSLCTKLCPLQIEN 161
DB 121 KQNTVCTCHAGFFLRENECVSCSNCKKSLCTKLCPLQIEN 161

RESULT 4
AAW89233
ID AAW89233 standard; Protein; 161 AA.
XX
AC AAW89233;
XX
DT 04-MAR-1999 (first entry)
XX
DE Tumour necrosis inhibitor 30 kDa protein.
XX
KW Tumour necrosis factor receptor 1; TNFR-1; inhibitor; osteoprotegerin;
KW OPG; chimeric; fusion; dimerisation domain; autoimmune disease;
KW inflammation; apoptosis.
XX
OS Homo sapiens.
XX
PN WO9849305-A1.
XX
PD 05-NOV-1998.
XX
PF 29-APR-1998; 98WO-US08631.
XX
PR 01-MAY-1997; 97US-0850188.
XX
PA (AMGE-) AMGEN INC.
XX
PI Boyle WJ, Wooden S;
XX
XX WPI; 1999-034661/03.
DR N-PSDB; AAW81732.
XX
XX New chimeric osteoprotegerin polypeptides - contain the
PT osteoprotegerin dimerisation domain and a heterologous sequence,
PT useful to treat TNF and TNFR-mediated disorders
XX
PS Disclosure; Fig 2; 92pp; English.
XX
XX The present invention describes a chimeric polypeptide (A1), comprising

an osteoprotegerin (OPG) dimerisation domain fused to a heterologous amino acid sequence. Also described are: (1) a multimer polypeptide comprising covalently associated Al monomers; (2) an isolated nucleic acid encoding Al; (3) an expression vector comprising the nucleic acid sequence; and (4) a host cell transformed or transfected with the expression vector so that the nucleic acid is expressible. The products from the present invention are useful to treat a variety of disorders including those related to receptor binding. Compositions comprising tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras are used to treat TNF and TNFR-mediated disorders such as inflammation, autoimmune diseases and disorders related to excessive apoptosis. The chimeras are also useful for detecting molecules which interact with fused heterologous sequences to identify potential new receptors and ligands. The present sequence represents the TNF inhibitor 30 kDa protein.

Query Match 100.0%; Score 941; DB 20; Length 161;
Best Local Similarity 100.0%; Pred. No. 2.4e-67;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVCPQGYIHPQNNISICTCKHKGTYLYNDPCPGQDTCRECSGSFTASENHLRHCL 60
DB 1 DSVCPQGYIHPQNNISICTCKHKGTYLYNDPCPGQDTCRECSGSFTASENHLRHCL 60

QY 61 SCSKCRKEMGQVEISSCTVDRDTCGCRKNQYRHWSENLFQCFNCSLCNGTVHLSQOE 120
DB 61 SCSKCRKEMGQVEISSCTVDRDTCGCRKNQYRHWSENLFQCFNCSLCNGTVHLSQOE 120

QY 121 KQNTVCTCHAGFFLRENECVSCSNCKKSLCTKLCPLQIEN 161
DB 121 KQNTVCTCHAGFFLRENECVSCSNCKKSLCTKLCPLQIEN 161

RESULT 5
AAB37676
ID AAB37676 standard; protein; 161 AA.
XX
AC AAB37676;
XX
DT 02-MAR-2001 (first entry)
XX
DE Human 30 kDa TNF inhibitor.
XX
KW TNF inhibitor; antiinflammatory; Tumour Necrosis Factor; interleukin;
KW IL-1; inflammatory disease; degenerative disease; human.
XX
OS Homo sapiens.
XX
PN US6143866-A.
XX
PD 07-NOV-2000.
XX
PF 19-JAN-1995; 95US-0375242.
XX
PR 19-JUL-1990; 90US-0555274.
PR 09-JUL-1993; 93US-0030366.
PR 18-JUL-1989; 89US-0381080.
PR 11-DEC-1989; 89US-0450329.
PR 07-FEB-1990; 90US-0479661.
XX
PA (AMGE-) AMGEN INC.
XX
XX Squires C, King MW, Hale KK, Brewer MT, Thompson RC;
PI Vanderslice RW, Vannice J, Kohno T;
XX
DR WPI; 2001-006443/01.
DR N-PSDB; AAC83945.
XX
XX Novel 30 kDa tumor necrosis factor inhibitor analog comprising a
PT non-native cysteine residue cross-linked with polyethylene glycol,
PT useful for treating inflammatory and degenerative diseases mediated by

PT TNF -
 XX Claim 1; Fig 19; 82pp; English.
 XX
 CC The present invention relates to Tumour Necrosis Factor (TNF) inhibitors
 CC (see AAB37676 and AAB37685), which have TNF inhibitory activity. The
 CC novel TNF inhibitors of the present invention are useful as therapeutic
 CC agents for inhibiting the activity of TNF and interleukin (IL-1), and
 CC for treating inflammatory and degenerative diseases mediated by TNF. The
 CC 30 kDa TNF inhibitor can inhibit TNF alpha.
 CC
 SQ Sequence 161 AA;
 Query March 100.0%; Score 941; DB 22; Length 161;
 Best Local Similarity 100.0%; Pred. No. 2.4e-67;
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DSVCPQGYIHPQNNISICTCKHKGTYLYNDPCPGQDTCRECESSGFTASENHLRHCL 60
 Db 1 DSVCPQGYIHPQNNISICTCKHKGTYLYNDPCPGQDTCRECESSGFTASENHLRHCL 60
 QY 61 SCSKCRKEMGVEISSCTVDRDVTVCGRKNQYRHWSNLFQCTNCSLCINGTVHLSQOE 120
 Db 61 SCSKCRKEMGVEISSCTVDRDVTVCGRKNQYRHWSNLFQCTNCSLCINGTVHLSQOE 120
 QY 121 KONTVCTCHAGFPLENECVSCSNCKSLLECTKLCPLPOIEN 161
 Db 121 KONTVCTCHAGFPLENECVSCSNCKSLLECTKLCPLPOIEN 161
 RESULT 6
 ID AAB89225 standard; Protein: 211 AA.
 XX AAB89225;
 AC
 XX AAW89225;
 DT 04-MAR-1999 (first entry)
 XX
 DE Tumour necrosis factor bp/osteoprotegerin construct TNFbp 4.0.
 XX
 KW Tumour necrosis factor receptor 1; TNFR-1; inhibitor; osteoprotegerin;
 KW OPG; chimeric; fusion; dimerisation domain; autoimmune disease;
 KW inflammation; apoptosis.
 XX Homo sapiens.
 OS Synthetic.
 XX
 PN WO9849305-A1.
 XX
 PD 05-NOV-1998.
 XX
 PF 29-APR-1998; 98WO-US08631.
 XX
 PR 01-MAY-1997; 97US-0850188.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Boyle WJ, Wooden S;
 XX
 DR WPI; 1999-034661/03.
 XX
 PT New chimeric osteoprotegerin polypeptides - contain the
 PT osteoprotegerin dimerisation domain and a heterologous sequence,
 PT useful to treat TNF and TNFR-mediated disorders
 XX
 PS Example 1; Fig 4; 92pp; English.
 CC The present invention describes a chimeric polypeptide (A1), comprising
 CC an osteoprotegerin (OPG) dimerisation domain fused to a heterologous
 CC amino acid sequence. Also described are: (1) a multimer polypeptide
 CC comprising covalently associated A1 monomers; (2) an isolated nucleic
 CC acid encoding A1; (3) an expression vector comprising the nucleic acid
 CC sequence; and (4) a host cell transformed or transfected with the

CC expression vector so that the nucleic acid is expressible. The products
 CC from the present invention are useful to treat a variety of disorders
 CC including those related to receptor binding. Compositions comprising
 CC tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras
 CC are used to treat TNF and TNFR-mediated disorders such as inflammation,
 CC autoimmune diseases and disorders related to excessive apoptosis. The
 CC chimeras are also useful for detecting molecules which interact with
 CC fused heterologous sequences to identify potential new receptors and
 CC ligands. The present sequence represents a TNFbp/OPG construct from
 CC the example of the present invention for creating TNFbp/OPG fusion
 CC proteins.
 CC
 SQ Sequence 211 AA;
 Query March 100.0%; Score 941; DB 20; Length 211;
 Best Local Similarity 100.0%; Pred. No. 3.1e-67;
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DSVCPQGYIHPQNNISICTCKHKGTYLYNDPCPGQDTCRECESSGFTASENHLRHCL 60
 Db 41 DSVCPQGYIHPQNNISICTCKHKGTYLYNDPCPGQDTCRECESSGFTASENHLRHCL 100
 QY 61 SCSKCRKEMGVEISSCTVDRDVTVCGRKNQYRHWSNLFQCTNCSLCINGTVHLSQOE 120
 Db 101 SCSKCRKEMGVEISSCTVDRDVTVCGRKNQYRHWSNLFQCTNCSLCINGTVHLSQOE 160
 QY 121 KONTVCTCHAGFPLENECVSCSNCKSLLECTKLCPLPOIEN 161
 Db 161 KONTVCTCHAGFPLENECVSCSNCKSLLECTKLCPLPOIEN 201
 RESULT 7
 ID AAB66979 standard; Protein: 280 AA.
 XX AAB66979;
 AC
 XX AAB66979;
 DT 19-APR-2001 (first entry)
 XX
 DE Tnf1 protein.
 XX
 KW Bone loss; osteoprotegerin; OPG; rheumatoid arthritis; hyperalgesia;
 KW multiple sclerosis; osteoporosis; osteomyelitis; asthma; inflammation;
 KW systemic lupus erythematosus; graft-versus-host disease; septic shock;
 KW acute pancreatitis; Alzheimer's disease; anorexia; atherosclerosis; pain;
 KW coronary condition; myocardial infarction; cancer; diabetes; psoriasis;
 KW endometriosis; fever; glomerulonephritis; inflammatory bowel disease;
 KW ischaemia; Parkinson's disease.
 XX
 OS Unidentified.
 XX
 PN WO200103719-A2.
 XX
 PD 18-JAN-2001.
 XX
 PF 07-JUL-2000; 2000WO-US18667.
 XX
 PR 09-JUL-1999; 99US-0350670.
 XX
 PR 09-DEC-1999; 99US-0457647.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Boyle WJ, Lacey DL, Calzone FJ, Chang M, Senaldi G;
 XX
 DR WPI; 2001-103031/11.
 XX
 PT Treating conditions leading to bone loss such as rheumatoid arthritis,
 PT multiple sclerosis and asthma, comprises administering an
 PT osteoprotegerin protein in conjunction with e.g. inhibitors of
 PT interleukin and tumor necrosis factor alpha
 XX
 PS Disclosure; Fig 2; 316pp; English.

CC The present invention relates to a method for treating conditions leading
 CC to bone loss. The method comprises administering a purified and isolated
 CC osteoprotegerin (OPG) protein (AAF57836-AAF57838 and AAB66974-AAB66976)
 CC in conjunction with other substances such as tumour necrosis factor- α
 CC (TNF- α) inhibitors, interleukin (IL)-6, -8 and -18 inhibitors, ICE
 CC modulators, fibroblast growth factor (FGF)-1-10 modulators and/or platelet
 CC activating factor (PAF) antagonists. The method is useful for treating
 CC conditions leading to bone loss such as rheumatoid arthritis, multiple
 CC sclerosis, osteoporosis, osteomyelitis and asthma. The method is also
 CC useful for treating inflammation, systemic lupus erythematosus (SLE) and
 CC graft-versus-host disease (GVHD). Other diseases that can be treated
 CC include acute pancreatitis, Alzheimer's disease, anorexia,
 CC atherosclerosis, coronary conditions (e.g. myocardial infarction),
 CC cancer, diabetes, endometriosis, fever, glomerulonephritis, hyperalgesia,
 CC inflammatory bowel disease, ischaemia, pain, Parkinson's disease,
 CC psoriasis and septic shock. The present sequence was used in a sequence
 CC homology comparison.

XX Sequence 280 AA;
 CC Query Match 100.0%; Score 941; DB 22; Length 280;
 CC Best Local Similarity 100.0%; Pred. No. 4e-67;
 CC Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DSVCPQGYIHPQNNISICTCKHGTLYNDPCPGQDTDCRECSGFTASENHLRCL 60
 DB 41 DSVCPQGYIHPQNNISICTCKHGTLYNDPCPGQDTDCRECSGFTASENHLRCL 100
 QY 61 SCSKCRKEMGQVEISSCTVDRDTCGCRKNQYRHWSENLFCQNCSLCLNGTVHLSQOE 120
 DB 101 SCSKCRKEMGQVEISSCTVDRDTCGCRKNQYRHWSENLFCQNCSLCLNGTVHLSQOE 160
 QY 121 KQNTVCTCHAGFFLRENECVSCNCKSLECTKLCPLQIEN 161
 DB 161 KQNTVCTCHAGFFLRENECVSCNCKSLECTKLCPLQIEN 201

RESULT 8
 ID AAR70108
 XX AAR70108 standard; Protein; 309 AA.
 AC AAR70108;
 DT 10-NOV-1995 (first entry)
 XX TNF-R-GBPH fusion protein.
 XX Hybrid peptide; malaria parasite; Plasmodium falciparum; fusion protein;
 KW red blood cell; cytokine receptor; glycophorin binding peptide 130;
 KW GBP 130; GBPH; glycophorin binding peptide homologue; glycophorin A;
 KW tumour necrosis factor receptor; TNF-R.
 XX Chimeric Homo sapiens.
 OS Chimeric Plasmodium falciparum.
 XX Key Location/Qualifiers
 FT Misc-difference 230..269
 FT /label= repeat region
 FT /note= "can be repeated n times, where n is a real
 FT number"
 XX WO9506737-A.
 FN 09-MAR-1995.
 PD 01-SEP-1994; 94WO-GB01900.
 PF 03-SEP-1993; 93GB-0018350.
 PR 23-AUG-1994; 94GB-0017021.
 XX (PREN/) PRENDERGAST K F.
 XX Prendergast KF;
 FI

XX WPI; 1995-115452/15.
 DR New hybrid peptide(s) for binding cytokine(s) - comprising a
 XX malaria parasite peptide capable of binding a red blood cell and
 PT a receptor peptide.
 XX Example A; Page 54-55; 93pp; English.
 XX Hybrid peptides for binding cytokines, comprising a malaria parasite
 CC (Plasmodium falciparum) peptide (capable of binding to a red blood
 CC cell (RBC)) and a receptor peptide are claimed. AAR70103-25 are examples
 CC of these hybrid peptides. AAR70108 is a fusion of tumour necrosis factor
 CC receptor (in accordance with H Loetscher et al Cell. Vol. 61, 351-359)
 CC and glycophorin binding protein (GBP) homologue (GBPH). The
 CC use of cytokine receptors not normally found on RBCs means that the
 CC cytokine can bind harmlessly to the RBC without deleterious effect.
 CC The RBC protects the hybrid peptides from excretion from the kidney, and
 CC due to steric hindrance prevents the cytokines binding to a receptor in
 CC another cell. GBP 130 or GBPH are the pref. malaria parasite peptides
 CC used, others include EBA 175 (175 kDa erythrocyte binding antigen),
 CC PMSA (pre major merozoite surface antigen) and the buffy binding
 CC receptor molecule (eg. exhibited by Plasmodium vivax). These peptides
 CC bind to pref. glycophorin A, B and C, sialo glycoproteins, found on the
 CC surface of RBCs. The hybrid peptides are thus used to lower the levels of
 CC free cytokines in the circulation to reduce pathological damage.
 XX Sequence 309 AA;
 SQ Query Match 100.0%; Score 941; DB 16; Length 309;
 CC Best Local Similarity 100.0%; Pred. No. 4.4e-67;
 CC Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DSVCPQGYIHPQNNISICTCKHGTLYNDPCPGQDTDCRECSGFTASENHLRCL 60
 DB 20 DSVCPQGYIHPQNNISICTCKHGTLYNDPCPGQDTDCRECSGFTASENHLRCL 79
 QY 61 SCSKCRKEMGQVEISSCTVDRDTCGCRKNQYRHWSENLFCQNCSLCLNGTVHLSQOE 120
 DB 80 SCSKCRKEMGQVEISSCTVDRDTCGCRKNQYRHWSENLFCQNCSLCLNGTVHLSQOE 139
 QY 121 KQNTVCTCHAGFFLRENECVSCNCKSLECTKLCPLQIEN 161
 DB 140 KQNTVCTCHAGFFLRENECVSCNCKSLECTKLCPLQIEN 180
 RESULT 9
 ID AAW89229
 XX AAW89229 standard; Protein; 311 AA.
 AC AAW89229;
 DT 04-MAR-1999 (first entry)
 XX Tumour necrosis factor bp/osteoprotegerin construct TNFbp/304.
 DE Tumour necrosis factor receptor 1; TNFR-1; inhibitor; osteoprotegerin;
 KW OPG; chimeric; fusion; dimerisation domain; autoimmune disease;
 KW inflammation; apoptosis.
 XX Homo sapiens.
 OS Synthetic.
 XX WO9849305-A1.
 FN 05-NOV-1998.
 PD 29-APR-1998; 98WO-US08631.
 PF 01-MAY-1997; 97US-0850188.
 PR (AMGE-) AMGEN INC.
 XX

PI Boyle WJ, Wooden S;
XX
DR WPI; 1999-034661/03.

XX New chimeric osteoprotegerin polypeptides - contain the
PT osteoprotegerin dimerisation domain and a heterologous sequence,
PT useful to treat TNF and TNFR-mediated disorders

XX Example 1; Fig 4; 92pp; English.

XX The present invention describes a chimeric polypeptide (A1), comprising
CC an osteoprotegerin (OPG) dimerisation domain fused to a heterologous
CC amino acid sequence. Also described are: (1) a multimer polypeptide
CC comprising covalently associated A1 monomers; (2) an isolated nucleic
CC acid encoding A1; (3) an expression vector comprising the nucleic acid
CC sequence; and (4) a host cell transformed or transfected with the
CC expression vector so that the nucleic acid is expressible. The products
CC from the present invention are useful to treat a variety of disorders
CC including those related to receptor binding. Compositions comprising
CC tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras
CC are used to treat TNF and TNFR-mediated disorders such as inflammation,
CC autoimmune diseases and disorders related to excessive apoptosis. The
CC chimeras are also useful for detecting molecules which interact with
CC fused heterologous sequences to identify potential new receptors and
CC ligands. The present sequence represents a TNFbp/OPG construct from
CC the example of the present invention for creating TNFbp/OPG fusion
CC proteins.

XX Sequence 311 AA;

Query Match 100.0%; Score 941; DB 20; Length 311;
Best Local Similarity 100.0%; Pred. No. 4.4e-67;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DSVCPQGYIHPNNSICTCTCHKGTLYLNDPQGDPTDCEESGSPFASENHLRHCL 60

DB 41 DSVCPQGYIHPNNSICTCTCHKGTLYLNDPQGDPTDCEESGSPFASENHLRHCL 100

OY 61 SCSKCRKEMGVEIISCTVDRDTCGCRKNQRYHWSNLFQCFNCSCLNGTVHLSQOE 120

DB 101 SCSKCRKEMGVEIISCTVDRDTCGCRKNQRYHWSNLFQCFNCSCLNGTVHLSQOE 160

OY 121 KONTVCTCHAGFFLENECVSCSNCKSLLECTKLCLEPIEN 161

DB 161 KONTVCTCHAGFFLENECVSCSNCKSLLECTKLCLEPIEN 201

RESULT 10
AAW33360
ID AAW33360 standard; Protein; 336 AA.

XX AAW33360;

XX 19-MAR-1998 (first entry)

XX TBP(20-190)/hCG-beta fusion protein.

XX Fusion protein; thrombopoietin; TPO; human chorionic gonadotrophin;

KW beta subunit; hCG-beta.

XX Homo sapiens.

XX MO9730161-A1.

XX 21-AUG-1997.

XX 20-FEB-1997; 97WO-US02315.

XX 20-FEB-1996; 96US-0011936.

XX (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.

XX Campbell RK, Chapel SC, Jameson BA;

XX WPI; 1997-425036/39.
DR N-PSDB; AAT94022.

XX Hybrid dimeric protein comprising two co-expressed units - each
PT based on receptor or ligand and a subunit of a heterodimeric
PT hormone, especially FSH, for inducing follicular maturation

XX Example; Pages 39-40; 60pp; English.

XX A novel fusion protein comprises 2 dimer forming co-expressed amino
CC acid sequences, each consisting of a homodimeric or heterodimeric
CC receptor chain or ligand, with ligand-receptor binding activity,
CC bound directly or via a peptide linker to a subunit of a
CC heterodimeric protein hormone capable of forming a heterodimer with
CC the hormone's other subunits. The fusion protein, e.g. the
CC thrombopoietin (TPO)/human chorionic gonadotrophin-beta subunit
CC (hCG-beta) fusion protein denoted by the present sequence,
CC significantly increases the biological activity of the hormone
CC component, reducing the requirement for hormone itself and the
CC number of injections needed.

XX Sequence 336 AA;

Query Match 100.0%; Score 941; DB 18; Length 336;
Best Local Similarity 100.0%; Pred. No. 4.7e-67;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DSVCPQGYIHPNNSICTCTCHKGTLYLNDPQGDPTDCEESGSPFASENHLRHCL 60

DB 23 DSVCPQGYIHPNNSICTCTCHKGTLYLNDPQGDPTDCEESGSPFASENHLRHCL 82

OY 61 SCSKCRKEMGVEIISCTVDRDTCGCRKNQRYHWSNLFQCFNCSCLNGTVHLSQOE 120

DB 83 SCSKCRKEMGVEIISCTVDRDTCGCRKNQRYHWSNLFQCFNCSCLNGTVHLSQOE 142

OY 121 KONTVCTCHAGFFLENECVSCSNCKSLLECTKLCLEPIEN 161

DB 143 KONTVCTCHAGFFLENECVSCSNCKSLLECTKLCLEPIEN 193

RESULT 11
AAW89228

ID AAW89228 standard; Protein; 366 AA.

XX AAW89228;

XX 04-MAR-1999 (first entry)

XX Tumour necrosis factor bp/osteoprotegerin construct TNFbp/248.

XX Tumour necrosis factor receptor 1; TNFR-1; inhibitor; osteoprotegerin;

KW OPG; chimeric; fusion; dimerisation domain; autoimmune disease;

XX inflammation; apoptosis.

XX Homo sapiens.

XX Synthetic.

XX WO9849305-A1.

XX 05-NOV-1998.

XX 29-APR-1998; 98WO-US08631.

XX 01-MAY-1997; 97US-0850188.

XX (AMGE-) AMGEN INC.

XX Boyle WJ, Wooden S;

XX WPI; 1999-034661/03.

XX New chimeric osteoprotegerin polypeptides - contain the

PT osteoprotegerin dimerisation domain and a heterologous sequence,
 XX useful to treat TNF and TNFR-mediated disorders
 PS Example 1; Fig 4; 92pp; English.
 XX
 CC The present invention describes a chimeric polypeptide (A1), comprising
 CC an osteoprotegerin (OPG) dimerisation domain fused to a heterologous
 CC amino acid sequence. Also described are: (1) a multimer polypeptide
 CC comprising covalently associated A1 monomers; (2) an isolated nucleic
 CC acid encoding A1; (3) an expression vector comprising the nucleic acid
 CC sequence; and (4) a host cell transformed or transfected with the
 CC expression vector so that the nucleic acid is expressible. The products
 CC from the present invention are useful to treat a variety of disorders
 CC including those related to receptor binding. Compositions comprising
 CC tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras
 CC are used to treat TNF and TNFR-mediated disorders such as inflammation,
 CC autoimmune diseases and disorders related to excessive apoptosis. The
 CC chimeras are also useful for detecting molecules which interact with
 CC fused heterologous sequences to identify potential new receptors and
 CC ligands. The present sequence represents a TNFbp/OPG construct from
 CC the example of the present invention for creating TNFbp/OPG fusion
 CC proteins.
 XX
 SQ Sequence 366 AA;
 Query Match 100.0%; Score 941; DB 20; Length 366;
 Best Local Similarity 100.0%; Pred. No. 5.1e-67;
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DSVCPQGYIHPQNNISICTCKHGTLYNDPCGPGQDTDCRECSGSFTASENHLRHCL 60
 DB 41 DSVCPQGYIHPQNNISICTCKHGTLYNDPCGPGQDTDCRECSGSFTASENHLRHCL 100
 QY 61 SCSKCRKEMGOVEISSCTVDRDTCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSQOE 120
 DB 101 SCSKCRKEMGOVEISSCTVDRDTCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSQOE 160
 QY 121 KQNTVCTCHAGFFLRENECVSCNCKSLECTKLCPLQIEN 161
 DB 161 KQNTVCTCHAGFFLRENECVSCNCKSLECTKLCPLQIEN 201
 RESULT 12
 AAR07449
 ID AAR07449 standard; protein; 371 AA.
 XX
 AC AAR07449;
 XX
 DT 29-JAN-1991 (first entry)
 XX
 DE Tumour Necrosis Factor-Binding Protein from pTNF-BP15 CDNA.
 XX
 KW Tumour necrosis factor binding protein; TNF-BP; TNF-receptor;
 KW pTNF-BP15; infectious disease; parasitic disease; cachexia;
 KW autoimmune disease; shock.
 XX
 OS Homo sapiens.
 XX
 PN EP393438-A.
 XX
 PD 24-OCT-1990.
 XX
 PF 06-APR-1990; 90EP-0106624.
 XX
 PR 21-JUN-1989; 89DE-3920282.
 PR 21-APR-1989; 89DE-3913101.
 XX
 PA (BOEH) BOEHRINGER INGELHEIMINT.
 XX
 PI Hauptmann R, Himmeler A, Maurer-Fogy I, Stratowa C;
 XX
 DR WPI; 1990-321987/43.
 DR N-PSDB; AAQ06282.

XX DNA encoding TNF binding protein and TNF-receptor - used in
 PT tumour treatment and to understand mechanism to TNF action
 XX
 PS Disclosure; Fig 1(1-3); 51pp; German.
 XX
 CC Clone pTNF-BP15 was used to construct pADTNF-BP, for transfection of
 CC e.g. COS7 cells. The expressed proteins are useful
 CC prophylactically and therapeutically to control disorders which
 CC involve the damaging effects of TNF-alpha or -beta (e.g. infectious or
 CC parasitic diseases, shock, cachexia, autoimmune diseases, adult
 CC respiratory distress syndrome etc., or side effects of treatment with
 CC TNF-alpha). They can also be used as diagnostic reagents for
 CC assaying TNF and in study of TNF-receptor interactions.
 CC See also AAQ06282-Q06285.
 XX
 SQ Sequence 371 AA;
 Query Match 100.0%; Score 941; DB 11; Length 371;
 Best Local Similarity 100.0%; Pred. No. 5.2e-67;
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DSVCPQGYIHPQNNISICTCKHGTLYNDPCGPGQDTDCRECSGSFTASENHLRHCL 60
 DB 41 DSVCPQGYIHPQNNISICTCKHGTLYNDPCGPGQDTDCRECSGSFTASENHLRHCL 100
 QY 61 SCSKCRKEMGOVEISSCTVDRDTCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSQOE 120
 DB 101 SCSKCRKEMGOVEISSCTVDRDTCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSQOE 160
 QY 121 KQNTVCTCHAGFFLRENECVSCNCKSLECTKLCPLQIEN 161
 DB 161 KQNTVCTCHAGFFLRENECVSCNCKSLECTKLCPLQIEN 201
 RESULT 13
 AAW89227
 ID AAW89227 standard; Protein; 397 AA.
 XX
 AC AAW89227;
 XX
 DT 04-MAR-1999 (first entry)
 XX
 DE Tumour necrosis factor bp/osteoprotegerin construct TNFbp/217.
 XX
 KW Tumour necrosis factor receptor 1; TNFR-1; inhibitor; osteoprotegerin;
 KW OPG; chimeric; fusion; dimerisation domain; autoimmune disease;
 KW inflammation; apoptosis.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO9849305-A1.
 XX
 PD 05-NOV-1998.
 XX
 PF 29-APR-1998; 98WO-US08631.
 XX
 PR 01-MAY-1997; 97US-0850188.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Boyle WJ, Wooden S;
 XX
 DR WPI; 1999-034661/03.
 XX
 PT New chimeric osteoprotegerin polypeptides - contain the
 PT osteoprotegerin dimerisation domain and a heterologous sequence,
 PT useful to treat TNF and TNFR-mediated disorders
 XX
 PS Example 1; Fig 4; 92pp; English.
 XX
 CC The present invention describes a chimeric polypeptide (A1), comprising

CC an osteoprotegerin (OPG) dimerisation domain fused to a heterologous
CC amino acid sequence. Also described are: (1) a multimer polypeptide
CC comprising covalently associated Al monomers; (2) an isolated nucleic
CC acid encoding Al; (3) an expression vector comprising the nucleic acid
CC sequence; and (4) a host cell transformed or transfected with the
CC expression vector so that the nucleic acid is expressible. The products
CC from the present invention are useful to treat a variety of disorders
CC including those related to receptor binding. Compositions comprising
CC tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras
CC are used to treat TNF and TNFR-mediated disorders such as inflammation,
CC autoimmune diseases and disorders related to excessive apoptosis. The
CC chimeras are also useful for detecting molecules which interact with
CC fused heterologous sequences to identify potential new receptors and
CC ligands. The present sequence represents a TNFbp/OPG construct from
CC the example of the present invention for creating TNFbp/OPG fusion
CC proteins.

XX Sequence 397 AA;

Query Match 100.0%; Score 941; DB 20; Length 397;
Best Local Similarity 100.0%; Pred. No. 5,5e-67;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVCPQKGIHPQNNISICTCKHGTLYLNDPCPGQDTCREBSGSFTASENHLRHCL 60

Db 41 DSVCPQKGIHPQNNISICTCKHGTLYLNDPCPGQDTCREBSGSFTASENHLRHCL 100

QY 61 SCSKCRKMGVEIISCTVDRTVCGCRKNQYRHWSENLFCQFNCSLCLNGTVHLSQOE 120

Db 101 SCSKCRKMGVEIISCTVDRTVCGCRKNQYRHWSENLFCQFNCSLCLNGTVHLSQOE 160

QY 121 KONTVCTCHAGFFLENECVSCSNCKSLLECTKLCPLPIEN 161

Db 161 KONTVCTCHAGFFLENECVSCSNCKSLLECTKLCPLPIEN 201

RESULT 14

AAW89226

ID AAW89226 standard; Protein; 417 AA.

XX AAW89226;

DT 04-MAR-1999 (first entry)

DE Tumour necrosis factor bp/osteoprotegerin construct TNFbp/196.

XX Tumour necrosis factor receptor 1; TNFR-1; inhibitor; osteoprotegerin;

KW OPG; chimeric; fusion; dimerisation domain; autoimmune disease;

KM inflammation; apoptosis.

XX Homo sapiens.

OS Synthetic.

XX WO9849305-A1.

XX 05-NOV-1998.

XX 29-APR-1998; 98WO-US08631.

XX 01-MAY-1997; 97US-0850188.

XX (AMGE-) AMGEN INC.

XX Boyle WJ, Wooden S;

XX WPI; 1999-034661/03.

XX New chimeric osteoprotegerin polypeptides - contain the

XX Example 1, Fig 4, 92pp; English.

CC The present invention describes a chimeric polypeptide (A1), comprising
CC an osteoprotegerin (OPG) dimerisation domain fused to a heterologous
CC amino acid sequence. Also described are: (1) a multimer polypeptide
CC comprising covalently associated Al monomers; (2) an isolated nucleic
CC acid encoding A1; (3) an expression vector comprising the nucleic acid
CC sequence; and (4) a host cell transformed or transfected with the
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CC including those related to receptor binding. Compositions comprising
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CC are used to treat TNF and TNFR-mediated disorders such as inflammation,
CC autoimmune diseases and disorders related to excessive apoptosis. The
CC chimeras are also useful for detecting molecules which interact with
CC fused heterologous sequences to identify potential new receptors and
CC ligands. The present sequence represents a TNFbp/OPG construct from
CC the example of the present invention for creating TNFbp/OPG fusion
CC proteins.

SQ Sequence 417 AA;

Query Match 100.0%; Score 941; DB 20; Length 417;
Best Local Similarity 100.0%; Pred. No. 5,8e-67;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVCPQKGIHPQNNISICTCKHGTLYLNDPCPGQDTCREBSGSFTASENHLRHCL 60

Db 41 DSVCPQKGIHPQNNISICTCKHGTLYLNDPCPGQDTCREBSGSFTASENHLRHCL 100

QY 61 SCSKCRKMGVEIISCTVDRTVCGCRKNQYRHWSENLFCQFNCSLCLNGTVHLSQOE 120

Db 101 SCSKCRKMGVEIISCTVDRTVCGCRKNQYRHWSENLFCQFNCSLCLNGTVHLSQOE 160

QY 121 KONTVCTCHAGFFLENECVSCSNCKSLLECTKLCPLPIEN 161

Db 161 KONTVCTCHAGFFLENECVSCSNCKSLLECTKLCPLPIEN 201

RESULT 15

AAW89224

ID AAW89224 standard; Protein; 420 AA.

XX AAW89224;

DT 04-MAR-1999 (first entry)

DE Tumour necrosis factor bp/osteoprotegerin construct TNFbp/OPG.

XX Tumour necrosis factor receptor 1; TNFR-1; inhibitor; osteoprotegerin;

KW OPG; chimeric; fusion; dimerisation domain; autoimmune disease;

KM inflammation; apoptosis.

XX Homo sapiens.

OS Synthetic.

XX WO9849305-A1.

XX 05-NOV-1998.

XX 29-APR-1998; 98WO-US08631.

XX 01-MAY-1997; 97US-0850188.

XX (AMGE-) AMGEN INC.

XX Boyle WJ, Wooden S;

XX WPI; 1999-034661/03.

XX New chimeric osteoprotegerin polypeptides - contain the

XX Example 1, Fig 4, 92pp; English.

XX The present invention describes a chimeric polypeptide (A1), comprising
CC an osteoprotegerin (OPG) dimerisation domain fused to a heterologous
CC amino acid sequence. Also described are: (1) a multimer polypeptide
CC comprising covalently associated A1 monomers; (2) an isolated nucleic
CC acid encoding A1; (3) an expression vector comprising the nucleic acid
CC sequence; and (4) a host cell transformed or transfected with the
CC expression vector so that the nucleic acid is expressible. The products
CC from the present invention are useful to treat a variety of disorders
CC including those related to receptor binding. Compositions comprising
CC tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras
CC are used to treat TNF and TNFR-mediated disorders such as inflammation,
CC autoimmune diseases and disorders related to excessive apoptosis. The
CC chimeras are also useful for detecting molecules which interact with
CC fused heterologous sequences to identify potential new receptors and
CC ligands. The present sequence represents a TNFbp/OPG construct from
CC the example of the present invention for creating TNFbp/OPG fusion
CC proteins.
XX

SQ Sequence 420 AA;

Query Match 100.0%; Score 941; DB 20; Length 420;
Best Local Similarity 100.0%; Pred. No. 5.8e-67;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DSVCPQGYIHPQNNISICTKCHKGTLYNDGPGQDTDCRECSGSFTASENHLRHCL 60
DB 41 DSVCPQGYIHPQNNISICTKCHKGTLYNDGPGQDTDCRECSGSFTASENHLRHCL 100
QY 61 SCSKCRKEMQVEISSCTVDRDTCGCRKQYRHYWSENLFQCFNCSLCLNGTVHLSQOE 120
DB 101 SCSKCRKEMQVEISSCTVDRDTCGCRKQYRHYWSENLFQCFNCSLCLNGTVHLSQOE 160
QY 121 KQNTVCTCHAGFFLRENECVSCNCKKSLECTKLCPLQIEN 161
DB 161 KQNTVCTCHAGFFLRENECVSCNCKKSLECTKLCPLQIEN 201

Search completed: December 3, 2002, 14:40:05
Job time : 37 secs

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OM protein - protein search, using sw model

Run on: December 3, 2002, 14:39:28 ; Search time 15 Seconds
(without alignments)
315.806 Million cell updates/sec

Title: US-09-907-263-2
Perfect score: 941
Sequence: 1 DSVCPQKVIHPQNSICCT.....CSNCKKSLCTKLCIPQIEN 161

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/1/iaa/5B COMB.pep: *
3: /cgn2_6/ptodata/1/iaa/6A COMB.pep: *
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5: /cgn2_6/ptodata/1/iaa/6C COMB.pep: *
6: /cgn2_6/ptodata/1/iaa/6D COMB.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	941	100.0	161	4	US-09-326-394-2
2	941	100.0	280	3	US-08-974-022-46
3	941	100.0	280	4	US-08-795-445A-46
4	941	100.0	280	4	US-08-795-447A-46
5	941	100.0	280	4	US-08-974-186-46
6	941	100.0	280	4	US-08-795-446B-46
7	941	100.0	280	4	US-08-706-945D-132
8	941	100.0	336	4	US-08-804-166-8
9	941	100.0	336	4	US-08-910-991-8
10	941	100.0	455	1	US-08-050-319B-25
11	941	100.0	455	1	US-08-321-668-2
12	941	100.0	455	1	US-08-837-941-2
13	941	100.0	455	2	US-08-126-016-2
14	941	100.0	455	2	US-08-465-982-25
15	941	100.0	455	4	US-08-815-469-5
16	941	100.0	455	4	US-09-006-353A-3
17	941	100.0	455	4	US-09-527-236A-5
18	941	100.0	455	4	US-08-054-970-2
19	941	100.0	455	4	US-09-565-918-4
20	941	100.0	455	4	US-09-573-986-3
21	930.5	98.9	909	4	US-09-013-895A-4
22	930.5	98.9	909	4	US-09-448-868-4
23	928	98.6	285	4	US-08-804-166-6
24	928	98.6	285	4	US-08-910-991-6
25	925.5	98.4	453	4	US-09-086-483A-5
26	924	98.2	199	1	US-08-050-319B-48
27	924	98.2	199	2	US-08-465-982-48

28	921	97.9	197	4	US-08-828-683A-21
29	904	96.1	154	4	US-08-828-683A-12
30	900	95.6	133	2	US-08-219-237B-4
31	900	95.6	133	4	US-08-477-347-12
32	900	95.6	153	4	US-08-476-862-3
33	900	95.6	153	4	US-08-468-560C-4
34	873	92.8	154	2	US-08-232-087A-10
35	842.5	89.5	256	4	US-08-804-166-2
36	842.5	89.5	256	4	US-08-910-991-2
37	837	88.9	307	4	US-08-804-166-4
38	837	88.9	307	4	US-08-910-991-4
39	822	87.4	139	4	US-08-706-945D-129
40	746	79.3	167	1	US-08-050-319B-2
41	746	79.3	167	1	US-08-050-319B-57
42	746	79.3	167	2	US-08-465-982-2
43	746	79.3	167	2	US-08-465-982-57
44	731	77.7	124	1	US-08-050-319B-4
45	731	77.7	124	2	US-08-465-982-4

ALIGNMENTS

RESULT 1
US-09-326-394-2
; Sequence 2, Application US/09326394
; Patent No. 6306820
; GENERAL INFORMATION:
; APPLICANT: Bendele, Alison M.
; APPLICANT: Sennello, Regina M.
; APPLICANT: Edwards, Carl K.
; TITLE OF INVENTION: COMBINATION THERAPY USING A TNF BINDING
; TITLE OF INVENTION: PROTEIN FOR TREATING TNF-MEDIATED DISEASES
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: CA
; COUNTRY: US
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/326,394
; FILING DATE: 08-DEC-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/032,587
; FILING DATE: 06-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,355
; FILING DATE: 23-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/039,315
; FILING DATE: 07-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/052,023
; FILING DATE: 09-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Zindrick, Thomas K.
; REGISTRATION NUMBER: 32,185
; REFERENCE/DOCKET NUMBER: A-430D
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 161 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-326-394-2

Query Match 100.0%; Score 941; DB 4; Length 161;
Best Local Similarity 100.0%; Pred. No. 1.6e-76;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVCPQGXVHPNNSICTCKHGTLYLNDPCPGQDTCRECESSFTASENHLRHCL 60
DB 1 DSVCPQGXVHPNNSICTCKHGTLYLNDPCPGQDTCRECESSFTASENHLRHCL 60
QY 61 SCSKCRKEMQVEISSCTVDRDTCGCRKNQRYHWSENLFCQCNCSLCNGTVHLSQOE 120
DB 61 SCSKCRKEMQVEISSCTVDRDTCGCRKNQRYHWSENLFCQCNCSLCNGTVHLSQOE 120
QY 121 KONTVCTCHAGFLRENECVSCSNCKKSLECTKCLPQIEN 161
DB 121 KONTVCTCHAGFLRENECVSCSNCKKSLECTKCLPQIEN 161

RESULT 2

US-08-974-022-46
Sequence 46, Application US/08974022
Patent No. 6015938
GENERAL INFORMATION:
APPLICANT: Boyle, William J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,022
FILING DATE: 12-DEC-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-378
INFORMATION FOR SEQ. ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 280 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-974-022-46

Query Match 100.0%; Score 941; DB 3; Length 280;
Best Local Similarity 100.0%; Pred. No. 2.7e-76;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVCPQGXVHPNNSICTCKHGTLYLNDPCPGQDTCRECESSFTASENHLRHCL 60
DB 41 DSVCPQGXVHPNNSICTCKHGTLYLNDPCPGQDTCRECESSFTASENHLRHCL 100
QY 61 SCSKCRKEMQVEISSCTVDRDTCGCRKNQRYHWSENLFCQCNCSLCNGTVHLSQOE 120
DB 101 SCSKCRKEMQVEISSCTVDRDTCGCRKNQRYHWSENLFCQCNCSLCNGTVHLSQOE 160
QY 121 KONTVCTCHAGFLRENECVSCSNCKKSLECTKCLPQIEN 161

DB 161 KONTVCTCHAGFLRENECVSCSNCKKSLECTKCLPQIEN 201

RESULT 3

US-08-795-445A-46
Sequence 46, Application US/08795445A
Patent No. 6284485
GENERAL INFORMATION:
APPLICANT: Boyle, William J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,445A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-378
INFORMATION FOR SEQ. ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 280 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-795-445A-46

Query Match 100.0%; Score 941; DB 4; Length 280;
Best Local Similarity 100.0%; Pred. No. 2.7e-76;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVCPQGXVHPNNSICTCKHGTLYLNDPCPGQDTCRECESSFTASENHLRHCL 60
DB 41 DSVCPQGXVHPNNSICTCKHGTLYLNDPCPGQDTCRECESSFTASENHLRHCL 100
QY 61 SCSKCRKEMQVEISSCTVDRDTCGCRKNQRYHWSENLFCQCNCSLCNGTVHLSQOE 120
DB 101 SCSKCRKEMQVEISSCTVDRDTCGCRKNQRYHWSENLFCQCNCSLCNGTVHLSQOE 160
QY 121 KONTVCTCHAGFLRENECVSCSNCKKSLECTKCLPQIEN 161
DB 161 KONTVCTCHAGFLRENECVSCSNCKKSLECTKCLPQIEN 201
RESULT 4
US-08-795-447A-46
Sequence 46, Application US/08795447A
Patent No. 6284728
GENERAL INFORMATION:
APPLICANT: Boyle, William J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: Osteoprotegerin

; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: One Amgen Center Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,447A
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378D2
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 280 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-795-447A-46

Query Match 100.0%; Score 941; DB 4; Length 280;
Best Local Similarity 100.0%; Pred. No. 2.7e-76;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSVCPQGYIHPQNNISCTCKCHKGTLYNDPCPGQDTCRECSGSFTASENHLRCL 60
Db 41 DSVCPQGYIHPQNNISCTCKCHKGTLYNDPCPGQDTCRECSGSFTASENHLRCL 100
Qy 61 SCSKCRKEMGOVEISSCTVDRTVCGCRKNQYRHYWSENLFQCFNCSCLNGTVHLSQOE 120
Db 101 SCSKCRKEMGOVEISSCTVDRTVCGCRKNQYRHYWSENLFQCFNCSCLNGTVHLSQOE 160
Qy 121 KONTVCTCHAGFFLRENECVSCNCKKSLECKLCLPQIEN 161
Db 161 KONTVCTCHAGFFLRENECVSCNCKKSLECKLCLPQIEN 201

RESULT 5

US-08-974-186-46
; Sequence 46, Application US/08974186
; Patent No. 6284740
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Behavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,186
; FILING DATE:
; CLASSIFICATION:

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 280 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-974-186-46

Query Match 100.0%; Score 941; DB 4; Length 280;
Best Local Similarity 100.0%; Pred. No. 2.7e-76;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSVCPQGYIHPQNNISCTCKCHKGTLYNDPCPGQDTCRECSGSFTASENHLRCL 60
Db 41 DSVCPQGYIHPQNNISCTCKCHKGTLYNDPCPGQDTCRECSGSFTASENHLRCL 100
Qy 61 SCSKCRKEMGOVEISSCTVDRTVCGCRKNQYRHYWSENLFQCFNCSCLNGTVHLSQOE 120
Db 101 SCSKCRKEMGOVEISSCTVDRTVCGCRKNQYRHYWSENLFQCFNCSCLNGTVHLSQOE 160
Qy 121 KONTVCTCHAGFFLRENECVSCNCKKSLECKLCLPQIEN 161
Db 161 KONTVCTCHAGFFLRENECVSCNCKKSLECKLCLPQIEN 201

RESULT 6

US-08-795-446B-46
; Sequence 46, Application US/08795446B
; Patent No. 6288032
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Behavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,446B
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 280 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-795-446B-46

Query Match 100.0%; Score 941; DB 4; Length 280;
Best Local Similarity 100.0%; Pred. No. 2.7e-76;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVCPGKXIHPPNNISICTCKHKGTYLYNDGPGQDTCRECEGSGFTASNNHRLHCL 60
DB 41 DSVCPGKXIHPPNNISICTCKHKGTYLYNDGPGQDTCRECEGSGFTASNNHRLHCL 100
QY 61 SCSKCKREMGOVEISSCTVDRDTCVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSOE 120
DB 101 SCSKCKREMGOVEISSCTVDRDTCVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSOE 160
QY 121 KONTVCTCHAGFFLRENECVSCSNCKKSLCTKLCUPOIEN 161
DB 161 KONTVCTCHAGFFLRENECVSCSNCKKSLCTKLCUPOIEN 201

RESULT 7
US-08-706-945D-132

; Sequence 132, Application US/08706945D
; Patent No. 6369027
; GENERAL INFORMATION:
; APPLICANT: Boyle, William
; APPLICANT: Lacey, David
; APPLICANT: Calzone, Frank
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: Osteoprotegerin
; FILE REFERENCE: A-378CIP
; CURRENT APPLICATION NUMBER: US/08/706,945D
; CURRENT FILING DATE: 1996-09-03
; PRIOR APPLICATION NUMBER: 08/577,788
; PRIOR FILING DATE: 1995-12-22
; NUMBER OF SEQ ID NOS: 145
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 132
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-706-945D-132

Query Match 100.0%; Score 941; DB 4; Length 280;
Best Local Similarity 100.0%; Pred. No. 2.7e-76;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVCPGKXIHPPNNISICTCKHKGTYLYNDGPGQDTCRECEGSGFTASNNHRLHCL 60
DB 41 DSVCPGKXIHPPNNISICTCKHKGTYLYNDGPGQDTCRECEGSGFTASNNHRLHCL 100
QY 61 SCSKCKREMGOVEISSCTVDRDTCVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSOE 120
DB 101 SCSKCKREMGOVEISSCTVDRDTCVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSOE 160
QY 121 KONTVCTCHAGFFLRENECVSCSNCKKSLCTKLCUPOIEN 161
DB 161 KONTVCTCHAGFFLRENECVSCSNCKKSLCTKLCUPOIEN 201

RESULT 8
US-08-804-166-8

; Sequence 8, Application US/08804166
; Patent No. 6193972
; GENERAL INFORMATION:
; APPLICANT: Campbell, Robert K.
; APPLICANT: Jameson, Bradford A.
; APPLICANT: Chappel, Scott C.
; TITLE OF INVENTION: HYBRID PROTEINS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.

COUNTRY: USA
ZIP: 22207
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,166
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/011,936
FILING DATE: 20 February 1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 336 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-804-166-8

Query Match 100.0%; Score 941; DB 4; Length 336;
Best Local Similarity 100.0%; Pred. No. 3.2e-76;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVCPGKXIHPPNNISICTCKHKGTYLYNDGPGQDTCRECEGSGFTASNNHRLHCL 60
DB 23 DSVCPGKXIHPPNNISICTCKHKGTYLYNDGPGQDTCRECEGSGFTASNNHRLHCL 82
QY 61 SCSKCKREMGOVEISSCTVDRDTCVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSOE 120
DB 83 SCSKCKREMGOVEISSCTVDRDTCVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSOE 142
QY 121 KONTVCTCHAGFFLRENECVSCSNCKKSLCTKLCUPOIEN 161
DB 143 KONTVCTCHAGFFLRENECVSCSNCKKSLCTKLCUPOIEN 183

RESULT 9
US-08-910-991-8

; Sequence 8, Application US/08910991
; Patent No. 6194177
; GENERAL INFORMATION:
; APPLICANT: Campbell, Robert K.
; APPLICANT: Jameson, Bradford A.
; APPLICANT: Chappel, Scott C.
; TITLE OF INVENTION: HYBRID PROTEINS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
ZIP: 22207
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,991
FILING DATE:
CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/804,166
FILING DATE: 20 February 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/011,936
FILING DATE: 20 February 1996
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: CAMPBELL=2B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 336 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-910-991-8

Query Match 100.0%; Score 941; DB 4; Length 336;
Best Local Similarity 100.0%; Pred. No. 3.2e-76;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSVCPQGYIHPQNNISCTCKCHKGTLYLYNDCPGQDTCRECEGSFTASENHLRHCL 60
Db 23 DSVCPQGYIHPQNNISCTCKCHKGTLYLYNDCPGQDTCRECEGSFTASENHLRHCL 82

Qy 61 SCSKCRKEMGQVEISSCTVDRDTCGCRKNQYRHYWSENLFQCFNCSCLNGTVHLSQOE 120
Db 83 SCSKCRKEMGQVEISSCTVDRDTCGCRKNQYRHYWSENLFQCFNCSCLNGTVHLSQOE 142

Qy 121 KONTVCTCHAGFFLRENECVSCSNCKKSLECKLCLPQIEN 161
Db 143 KONTVCTCHAGFFLRENECVSCSNCKKSLECKLCLPQIEN 183

RESULT 10
US-08-050-319B-25
Sequence 25, Application US/08050319B
Patent No. 5633145
GENERAL INFORMATION:
APPLICANT: M. Feldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.M. Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
Necrosis Factor alpha) Receptor
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Reed & Robbins
STREET: 635 Bryant Street
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/050,319B
FILING DATE: 10-May-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Robbins, Roberta L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5150-0030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:

LENGTH: 455 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-050-319B-25

Query Match 100.0%; Score 941; DB 1; Length 455;
Best Local Similarity 100.0%; Pred. No. 4.3e-76;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSVCPQGYIHPQNNISCTCKCHKGTLYLYNDCPGQDTCRECEGSFTASENHLRHCL 60
Db 41 DSVCPQGYIHPQNNISCTCKCHKGTLYLYNDCPGQDTCRECEGSFTASENHLRHCL 100

Qy 61 SCSKCRKEMGQVEISSCTVDRDTCGCRKNQYRHYWSENLFQCFNCSCLNGTVHLSQOE 120
Db 101 SCSKCRKEMGQVEISSCTVDRDTCGCRKNQYRHYWSENLFQCFNCSCLNGTVHLSQOE 160

Qy 121 KONTVCTCHAGFFLRENECVSCSNCKKSLECKLCLPQIEN 161
Db 161 KONTVCTCHAGFFLRENECVSCSNCKKSLECKLCLPQIEN 201

RESULT 11
US-08-321-668-2
Sequence 2, Application US/08321668
Patent No. 5655859
GENERAL INFORMATION:
APPLICANT: WALLACH, David
APPLICANT: BRAKEBUSCH, Cord
APPLICANT: VARFOLOMEEV, Eugene
APPLICANT: BATKIN, Michael
TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF
TITLE OF INVENTION: THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/321,668
FILING DATE: 12-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 107268
FILING DATE: 12-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WALLACH=13
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 455 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-321-668-2

Query Match 100.0%; Score 941; DB 1; Length 455;
Best Local Similarity 100.0%; Pred. No. 4.3e-76;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVCPQGYIHPONNSICTCKHGYLYNDGPGGDDTCRCBESSGFTASNNHLRCL 60
DB 41 DSVCPQGYIHPONNSICTCKHGYLYNDGPGGDDTCRCBESSGFTASNNHLRCL 100
QY 61 SCSKREMGQVEISSCTVDRTVCGCRKNQRYHWSNLFQCFNCSCLNGTVHLSOE 120
DB 101 SCSKREMGQVEISSCTVDRTVCGCRKNQRYHWSNLFQCFNCSCLNGTVHLSOE 160
QY 121 KONTVCTCHAGFLRENECVSCSNCKSLLECTKLCPLQIEN 161
DB 161 KONTVCTCHAGFLRENECVSCSNCKSLLECTKLCPLQIEN 201

RESULT 12
US-08-837-941-2
Sequence 2, Application US/08837941
Patent No. 5766917
GENERAL INFORMATION:
APPLICANT: WALLACH, David
APPLICANT: BRAKEBUSCH, Cord
APPLICANT: VARFOLOMEV, Eugene
APPLICANT: BATKIN, Michael
TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF
TITLE OF INVENTION: THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/837,941
FILING DATE: 28-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/321,668
FILING DATE: 12-OCT-1994
APPLICATION NUMBER: IT 107268
FILING DATE: 12-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WALLACH=13
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 455 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-837-941-2

Query Match 100.0%; Score 941; DB 1; Length 455;
Best Local Similarity 100.0%; Pred. No. 4.3e-76;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVCPQGYIHPONNSICTCKHGYLYNDGPGGDDTCRCBESSGFTASNNHLRCL 60
DB 41 DSVCPQGYIHPONNSICTCKHGYLYNDGPGGDDTCRCBESSGFTASNNHLRCL 100
QY 61 SCSKREMGQVEISSCTVDRTVCGCRKNQRYHWSNLFQCFNCSCLNGTVHLSOE 120
DB 161 KONTVCTCHAGFLRENECVSCSNCKSLLECTKLCPLQIEN 201

DB 101 SCSKREMGQVEISSCTVDRTVCGCRKNQRYHWSNLFQCFNCSCLNGTVHLSOE 160
QY 121 KONTVCTCHAGFLRENECVSCSNCKSLLECTKLCPLQIEN 161
DB 161 KONTVCTCHAGFLRENECVSCSNCKSLLECTKLCPLQIEN 201

RESULT 13
US-08-126-016-2
Sequence 2, Application US/08126016
Patent No. 5811261
GENERAL INFORMATION:
APPLICANT: WALLACH, DAVID
APPLICANT: NOPAR, YARON
APPLICANT: KEMPER, OLIVER
APPLICANT: ENGELMANN, HARTMUT
APPLICANT: BRAKEBUSCH, CORD
APPLICANT: ADERKA, DAN
TITLE OF INVENTION: EXPRESSION OF THE RECOMBINANT TUMOR
TITLE OF INVENTION: NECROSIS FACTOR BINDING PROTEIN I (TNF-1)
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/126,016
FILING DATE: 24-SEP-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/625668
FILING DATE: 13-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WALLACH4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 455 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-126-016-2

Query Match 100.0%; Score 941; DB 2; Length 455;
Best Local Similarity 100.0%; Pred. No. 4.3e-76;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVCPQGYIHPONNSICTCKHGYLYNDGPGGDDTCRCBESSGFTASNNHLRCL 60
DB 41 DSVCPQGYIHPONNSICTCKHGYLYNDGPGGDDTCRCBESSGFTASNNHLRCL 100
QY 61 SCSKREMGQVEISSCTVDRTVCGCRKNQRYHWSNLFQCFNCSCLNGTVHLSOE 120
DB 101 SCSKREMGQVEISSCTVDRTVCGCRKNQRYHWSNLFQCFNCSCLNGTVHLSOE 160
QY 121 KONTVCTCHAGFLRENECVSCSNCKSLLECTKLCPLQIEN 161
DB 161 KONTVCTCHAGFLRENECVSCSNCKSLLECTKLCPLQIEN 201

RESULT 14

US-08-465-982-25
; Sequence 25, Application US/08465982
; Patent No. 5863786
; GENERAL INFORMATION:
; APPLICANT: M.Feldmann, P.W. Gray,
; APPLICANT: M.J.C. Turner, F.W. Brennan
; TITLE OF INVENTION: Modified human TNFalpha (Tumor
; TITLE OF INVENTION: Necrosis Factor alpha) Receptor
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Reed & Robbins
; STREET: 635 Bryant Street
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,982
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/050,319
; FILING DATE: 10-May-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Robbins, Roberta L.
; REGISTRATION NUMBER: 33,208
; REFERENCE/DOCKET NUMBER: 5150-0030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 617-8999
; TELEFAX: (415) 327-3231
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 455 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-465-982-25

Query Match 100.0%; Score 941; DB 2; Length 455;

Best Local Similarity 100.0%; Pred. No. 4.3e-76;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSVCPQGYIHPQNNISICTCKHGTLYNDPCPGQDTCRECSGSFTASENHLRCL 60
|||
Db 41 DSVCPQGYIHPQNNISICTCKHGTLYNDPCPGQDTCRECSGSFTASENHLRCL 100
Qy 61 SCSKCRKEMGQVEISSCTVDRDTVCGRKNQYRHYWSENLFQCFNCSCLNGTVHLSQOE 120
|||
Db 101 SCSKCRKEMGQVEISSCTVDRDTVCGRKNQYRHYWSENLFQCFNCSCLNGTVHLSQOE 160
Qy 121 KONTVCTCHAGFFLRNECVSCSNCKKSLCTKLCPLQIEN 161
|||
Db 161 KONTVCTCHAGFFLRNECVSCSNCKKSLCTKLCPLQIEN 201

RESULT 15

US-08-815-469-5
; Sequence 5, Application US/08815469
; Patent No. 6153402
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ni, Jian
; APPLICANT: Dixit, Vishva
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Dillon, Patrick J.
; TITLE OF INVENTION: Death Domain Containing Receptors
; NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., NW, Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/815,469
; FILING DATE: HEREWITH
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: No. 6153402 Yet Assigned
; FILING DATE: 06-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/028,711
; FILING DATE: 17-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,285
; FILING DATE: 12-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 455 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; US-08-815-469-5

Query Match 100.0%; Score 941; DB 4; Length 455;

Best Local Similarity 100.0%; Pred. No. 4.3e-76;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSVCPQGYIHPQNNISICTCKHGTLYNDPCPGQDTCRECSGSFTASENHLRCL 60
|||
Db 41 DSVCPQGYIHPQNNISICTCKHGTLYNDPCPGQDTCRECSGSFTASENHLRCL 100
Qy 61 SCSKCRKEMGQVEISSCTVDRDTVCGRKNQYRHYWSENLFQCFNCSCLNGTVHLSQOE 120
|||
Db 101 SCSKCRKEMGQVEISSCTVDRDTVCGRKNQYRHYWSENLFQCFNCSCLNGTVHLSQOE 160
Qy 121 KONTVCTCHAGFFLRNECVSCSNCKKSLCTKLCPLQIEN 161
|||
Db 161 KONTVCTCHAGFFLRNECVSCSNCKKSLCTKLCPLQIEN 201

Search completed: December 3, 2002, 14:41:46
Job time : 16 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 3, 2002, 14:39:03 ; Search time 17 Seconds
(without alignments)
910.450 Million cell updates/sec

Title: US-09-907-263-2

Perfect score: 941

Sequence: 1 DSVCPQGYKIHQNNSICT.....CSNCKSELEKLCPLQIEN 161

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 73.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	941	100.0	455	1	GQHUT1
2	716.5	76.1	461	2	tumor necrosis fac
3	680	72.3	454	1	tumor necrosis fac
4	669	71.1	461	1	tumor necrosis fac
5	187.5	19.9	435	2	tumor necrosis fac
6	182.5	19.4	427	1	tumor necrosis fac
7	181	19.2	474	2	nerve growth facto
8	179.5	19.1	326	1	tumor necrosis fac
9	178	18.9	325	2	T2 protein - myxom
10	176.5	18.8	425	1	T2 protein - rabbi
11	176	18.7	459	2	nerve growth facto
12	167.5	17.8	305	2	Gene murine tumour
13	166.5	17.7	349	2	B cell-associated
14	164	17.4	348	2	G2R protein - vari
15	164	17.4	349	2	hypothetical prote
16	162.5	17.3	327	2	gene G4R protein -
17	161	17.1	461	1	apoptosis-mediati
18	158.5	16.8	651	2	tumor necrosis fac
19	147.5	15.7	677	2	death receptor-6
20	147	15.6	324	2	trophozoite cystei
21	145	15.4	416	1	Fas antigen precu
22	141	15.0	1680	2	nerve growth facto
23	139.5	14.8	250	1	furin EC 3.4.21.7
24	139.5	14.8	260	1	CD27 antigen precu
25	139.5	14.8	277	2	CD27 antigen precu
26	134	14.2	1548	2	B-cell activation
27	132	14.0	899	2	serine proteinase
28	132	14.0	915	2	subtilisin-like pr
29	131.5	14.0	272	2	subtilisin-like pr
					gene ox40 protein

ALIGNMENTS

RESULT 1

GQHUT1

tumor necrosis factor receptor 1 precursor [validated] - human

N:Alternate names: P55 tumor necrosis factor receptor; TNF receptor type 1

C:Contains: tumor necrosis factor alpha inhibitor; tumor necrosis factor binding protein

C:Species: Homo sapiens (man)

C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text change 08-Dec-2000

C:Accession: A38208; A34899; A34900; A36555; C36555; A38281; S12057; JT0758; A60231; A38:

R:Fuchs, P.; Strehl, S.; Dworzak, M.; Himmler, A.; Ambros, P.F.

Genomics 13, 219-224, 1992

A:Title: Structure of the human TNF receptor 1 (p60) gene (TNFRF1) and localization to chi

A:Reference number: A38208; MUID:92250049; PMID:1315717

A:Accession: A38208

A:Molecule type: DNA

A:Residues: 1-455 <FUC>

A:Cross-references: GB:M75864; GB:M75865; GB:M75866; NID:G339748; PIDN:AAA61201.1; PID:G:

R:Loetscher, H.; Pan, Y.C.E.; Lahm, H.W.; Gentz, R.; Brockhaus, M.; Tabuchi, H.; Lesslau

Cell 61, 351-359, 1990

A:Title: Molecular cloning and expression of the human 55 kd tumor necrosis factor recept

A:Reference number: A34899; MUID:90235284; PMID:2158862

A:Accession: A34899

A:Molecule type: mRNA

A:Residues: 1-455 <LOS>

A:Cross-references: GB:M58286; GB:M33480; NID:G339753; PIDN:AAA36753.1; PID:G339754

A:Experimental source: placenta

A>Note: part of this sequence, including the amino end of the mature protein, confirmed i

R:Schall, T.J.; Lewis, M.; Koller, K.J.; Lee, A.; Rice, G.C.; Wong, G.H.W.; Gatanaga, T.;

Cell 61, 361-370, 1990

A:Title: Molecular cloning and expression of a receptor for human tumor necrosis factor.

A:Reference number: A34900; MUID:90235285; PMID:2158863

A:Accession: A34900

A:Molecule type: mRNA

A:Residues: 1-455 <SCH>

A:Cross-references: GB:M33294; NID:G339744; PIDN:AAA03210.1; PID:G339745

R:Himmeler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.; Pfizenmaier, K.; Lantz, M.; C

DNA Cell Biol. 9, 705-715, 1990

A:Title: Molecular cloning and expression of human and rat tumor necrosis factor recepto

A:Reference number: A36555; MUID:91090841; PMID:1702293

A:Accession: A36555

A:Molecule type: mRNA

A:Residues: 1-455 <HIM>

A:Cross-references: GB:M63121; NID:G339755; PIDN:AAA36754.1; PID:G339756

A:Accession: C36555

A:Molecule type: protein

A:Residues: 30-38;41-53, 'X', '55-79, 'XX', '82-94, 'NK', '100-104;107-128;162-167, 'X', '169-20

A>Note: the purified protein, called tumor necrosis factor binding protein, is a soluble

R:Gray, P.W.; Barrett, K.; Chantray, D.; Turner, M.; Feldmann, M.

Proc. Natl. Acad. Sci. U.S.A. 87, 7380-7384, 1990

A:Title: Cloning of human tumor necrosis factor (TNF) receptor cDNA and expression of rec

A:Reference number: A38281; MUID:91017509; PMID:2170974

A:Accession: A38281

A:Molecule type: mRNA

A:Residues: 1-455 <GRA>
 A:Cross-references: GB:M37764
 A:Note: the authors translated the codon TCG for residue 371 as Thr, AAG for residue 372
 R:Kempner, Y.; Kempner, O.; Brakelbusch, C.; Engelmann, H.; Zhang, R.; Aderka, D.; Holtmann
 EMO J. 9, 3689-3278, 1990
 A:Title: Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA for the type
 1 form of the receptor.
 A:Reference number: S12057; MUID:91006021; PMID:1698610
 A:Accession: S12057
 A:Molecule type: mRNA
 A:Residues: 1-455 <NOP>
 A:Cross-references: EMBL:X55313; NID:g37223; PIDD:CA39021.1; PID:g37224
 A:Note: parts of soluble TNF binding protein 1, including its amino and carboxyl ends, w
 R:Kempner, O.; Wallach, D.
 Gene 134, 209-216, 1993
 A:Title: Cloning and partial characterization of the promoter for the human p55 tumor ne
 A:Reference number: J70758; MUID:94085779; PMID:8262379
 A:Accession: J70758
 A:Molecule type: DNA
 A:Residues: 1-13 <KEM>
 R:Secklinger, P.; Vey, E.; Turcatti, G.; Wingfield, P.; Dayer, J.M.
 Eur. J. Immunol. 20, 1167-1174, 1990
 A:Title: Tumor necrosis factor inhibitor: purification, NH-2-terminal amino acid sequenc
 A:Reference number: A60231; MUID:90292116; PMID:2113477
 A:Accession: A60231
 A:Molecule type: Protein
 A:Residues: 41-43, 'X', 45-53, 'X', 55-57 <SEC>
 R:Gatanaga, T.; Hwang, C.; Kohr, W.; Cappuccini, F.; Lucchi III, J.A.; Jeffes, E.W.B.; Le
 Proc. Natl. Acad. Sci. U.S.A. 87, 8781-8784, 1990
 A:Title: Purification and characterization of an inhibitor (soluble tumor necrosis facto
 A:Reference number: A38258; MUID:91062364; PMID:2174164
 A:Accession: A38258
 A:Molecule type: Protein
 A:Residues: 41-60 <GAT>
 A:Experimental source: cancer patient serum
 R:Olsson, I.; Lantzy, M.; Nilsson, E.; Peetre, C.; Thysell, H.; Grubb, A.; Adolf, G.
 Eur. J. Haematol. 42, 270-275, 1999
 A:Title: Isolation and characterization of a tumor necrosis factor binding protein from
 A:Reference number: A60594; MUID:89171156; PMID:2924890
 A:Accession: A60594
 A:Molecule type: Protein
 A:Residues: 41-43, 'X', 45-53, 'V', 55-57, 'X', 60 <OLS>
 R:Engelmann, H.; Novick, D.; Wallach, D.
 J. Biol. Chem. 265, 1531-1536, 1990
 A:Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence
 A:Reference number: A35010; MUID:90110215; PMID:2153136
 A:Accession: A35010
 A:Molecule type: Protein
 A:Residues: 41-45 <ENG>
 A:Experimental source: normal urine
 R:Kojihara, J.; Asada, A.; Kirihara, S.; Kato, K.
 Biosci. Biotechnol. Biochem. 58, 2266-2268, 1994
 A:Title: Amino acid sequence of natural tumor necrosis factor alpha inhibitor purified f
 A:Reference number: JC2404; MUID:95128033; PMID:7765720
 A:Accession: JC2404
 A:Molecule type: Protein
 A:Residues: 41-53, 'X', 55-144, 'X', 146-150, 'X', 152-186, 'X', 188-201 <KAJ>
 A:Experimental source: urine
 C:Comment: This protein is one of two known receptors for both TNF-alpha (cachectin) and
 C:Genetics:
 A:Gene: GDB:TNFR1
 A:Cross-references: GDB:125913; OMIM:191190
 A:Map position: 12p13.2-12p13.2
 A:Introns: 13/3; 65/1; 108/1; 158/1; 184/2; 209/1; 247/1; 256/3; 353/1
 C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
 C:Keywords: duplication; glycoprotein; receptor; transmembrane protein
 F:1-21/Domain: signal sequence #status predicted <SIG>
 F:22-45/Domain: signal sequence #status predicted <SIG>
 F:30-211/Domain: extracellular #status predicted <EXT>
 F:41-201/Domain: TNF binding protein 1 (tumor necrosis factor alpha inhibitor) #status
 F:44-82/Domain: NGF receptor repeat homology <NG1>

F:84-126/Domain: NGF receptor repeat homology <NG2>
 F:127-167/Domain: NGF receptor repeat homology <NG3>
 F:168-196/Domain: NGF receptor repeat homology <NG4>
 F:212-234/Domain: transmembrane #status predicted <MEM>
 F:235-455/Domain: intracellular #status predicted <INT>
 F:54,145,151/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 941; DB 1; Length 455;
 Best Local Similarity 100.0%; Pred. No. 8,3e-62;
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVCPQKXIHPPNNNSICCTKCHKGTLYNDPCPGQDPTDCRECSGSFTASENHLRHCL 60
 DB 41 DSVCPQKXIHPPNNNSICCTKCHKGTLYNDPCPGQDPTDCRECSGSFTASENHLRHCL 100

QY 61 SCSKCRKEMGVLEISCTVDRTVCGCRKNQYRHWSENLFOCFNCSLCINGVHLSQCE 120
 DB 101 SCSKCRKEMGVLEISCTVDRTVCGCRKNQYRHWSENLFOCFNCSLCINGVHLSQCE 160

QY 121 KONTVCTCHAGFLRENECVSCNCKSLBECTKCLPQIEN 161
 DB 161 KONTVCTCHAGFLRENECVSCNCKSLBECTKCLPQIEN 201

RESULT 2
 JC4302
 tumor necrosis factor receptor p55 precursor - pig
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 29-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 23-Jul-1999
 A:Accession: JC4302; PC4093
 R:Suter, B.; Paul, U.
 Gene 163, 263-266, 1995
 A:Title: Cloning of the cDNA encoding the porcine p55 tumor necrosis factor receptor.
 A:Reference number: JC4302; MUID:96011645; PMID:7590278
 A:Accession: JC4302
 A:Molecule type: mRNA
 A:Residues: 1-461 <SUT>
 A:Cross-references: GB:U19994; NID:g1141752; PIDD:AA48499.1; PID:g1141753
 A:Accession: PC4093
 A:Molecule type: Protein
 A:Residues: 1-7 <SUT>
 A:Experimental source: kidney cell line 15
 C:Genetics:
 A:Gene: tnfr
 C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
 C:Keywords: glycoprotein; kidney; receptor; transmembrane protein; tumor
 F:1-29/Domain: signal sequence #status predicted <SIG>
 F:30-461/Domain: product: tumor necrosis factor receptor p55 #status predicted <MAT>
 F:44-194/Domain: extracellular cysteine rich #status predicted <EXT>
 F:44-82/Domain: NGF receptor repeat homology <NG1>
 F:84-126/Domain: NGF receptor repeat homology <NGF>
 F:211-231/Domain: transmembrane #status predicted <TM>
 F:361-447/Domain: signal transduction #status predicted <SIT>
 F:54,145,151/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 76.1%; Score 716.5; DB 2; Length 461;
 Best Local Similarity 77.4%; Pred. No. 2e-45;
 Matches 120; Conservative 12; Mismatches 22; Indels 1; Gaps 1;

QY 1 DSVCPQKXIHPPNNNSICCTKCHKGTLYNDPCPGQDPTDCRECSGSFTASENHLRHCL 60
 DB 41 DSVCPQKXIHPPNNNSICCTKCHKGTLYNDPCPGQDPTDCRECSGSFTASENHLRHCL 100

QY 61 SCSKCRKEMGVLEISCTVDRTVCGCRKNQYRHWSENLFOCFNCSLCINGVHLSQCE 120
 DB 101 SCSKCRKEMGVLEISCTVDRTVCGCRKNQYRHWSENLFOCFNCSLCINGVHLSQCE 160

QY 121 KONTVCTCHAGFLRENECVSCNCKSLBECTKCLPQIEN 155
 DB 161 KONTVCTCHAGFLRENECVSCNCKSLBECTKCLPQIEN 194

RESULT 3

GOMSTI

tumor necrosis factor receptor 1 precursor - mouse
 N:Alternate names: tumor necrosis factor receptor, 55K
 C:Species: Mus musculus (house mouse)
 C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 01-Dec-2000
 C:Accession: A38634; B40254; S16677; S19021; I54532; I57826
 R:Lewis, M.; Tartagat, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, E.
 Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991
 A>Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis factor
 A:Reference number: A38634; MUID:91187885; PMID:1849278
 A:Accession: A38634
 A:Molecule type: mRNA
 A:Residues: 1-454 <LEW>
 A:Cross-references: GB:M60468; NID:G199825; PIDN:AAA39751.1; PID:G199826
 R:Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jenk
 Mol. Cell. Biol. 11, 3020-3026, 1991
 A>Title: Molecular cloning and expression of the type 1 and type 2 murine receptors for
 A:Reference number: A40254; MUID:91246168; PMID:1645445
 A:Accession: B40254
 A:Molecule type: mRNA
 A:Residues: 1-454 <GO2>
 A:Cross-references: GB:M60468; NID:G199825; PIDN:AAA39751.1; PID:G199826
 R:Barrett, K.; Taylor-Fishwick, D.A.; Cope, A.P.; Kissenerghis, A.M.; Gray, P.W.; Feldma
 Eur. J. Immunol. 21, 1649-1656, 1991
 A>Title: Cloning, expression and cross-linking analysis of the murine p55 tumor necrosis
 A:Reference number: S16677; MUID:91285014; PMID:1647956
 A:Accession: S16677
 A:Molecule type: mRNA
 A:Residues: 1-454 <BAR>
 A:Cross-references: EMBL:X59238; NID:G53578; PIDN:CAA41922.1; PID:G53579
 R:Rothe, J.G.; Brockhaus, M.; Gentz, R.; Lesslauer, W.
 Immunogenetics 34, 338-340, 1991
 A>Title: Molecular cloning and expression of the mouse Tnf receptor type b.
 A:Reference number: S19021; MUID:92039815; PMID:1657766
 A:Accession: S19021
 A:Molecule type: mRNA
 A:Residues: 1-454 <ROT>
 A:Cross-references: EMBL:X57796; NID:G54848; PIDN:CAA40936.1; PID:G54849
 R:Bebo, B.F.
 Immunogenetics 39, 450-451, 1994
 A>Title: Nucleotide sequence of the TNF type I receptor from a mouse endothelioma cell
 A:Reference number: I54532; MUID:94245292; PMID:8188324
 A:Accession: I54532
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-454 <RES>
 A:Cross-references: GB:L26349; NID:G430732; PIDN:AAA59361.1; PID:G430733
 R:Rothe, J.G.; Bluethmann, H.; Gentz, R.; Lesslauer, W.; Steinmetz, M.
 Mol. Immunol. 30, 165-176, 1993
 A>Title: Genomic organization and promoter function of the murine tumor necrosis factor
 A:Reference number: I57826; MUID:93156721; PMID:8381516
 A:Accession: I57826
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-393, 'G', 395-454 <RE2>
 A:Cross-references: GB:W76656; NID:G202100; PIDN:AAA40465.1; PID:G202102
 C:Comment: This protein is one of two distantly related receptors for both TNF-alpha (ca
 C:Genetics:
 A:Gene: TNFR-2
 A:Introns: 13/3; 65/1; 108/1; 158/1; 184/2; 210/1; 248/1; 257/3; 353/1
 C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
 C:Keywords: cytokine receptor; duplication; glycoprotein; receptor; transmembrane protei
 F:1-29/Domain: signal sequence #status predicted <SIG>
 F:30-454/Product: tumor necrosis factor receptor type 1 #status predicted <WAT>
 F:30-212/Domain: extracellular #status predicted <EXT>
 F:44-82/Domain: NGF receptor repeat homology <NG1>
 F:84-126/Domain: NGF receptor repeat homology <NG2>
 F:127-167/Domain: NGF receptor repeat homology <NG3>
 F:168-204/Domain: NGF receptor repeat homology <NG4>
 F:213-235/Domain: transmembrane #status predicted <MEM>
 F:236-454/Domain: intracellular #status predicted <INT>
 F:54,151,202/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 72.3%; Score 680; DB 1; Length 454;
 Best Local Similarity 71.3%; Pred. No. 9.1e-43;
 Matches 112; Conservative 19; Mismatches 26; Indels 0; Gaps 0;
 QY 1 DSVCPQGYIHPNNISICTCKHKGTYLYNDPCPGQDTCRECSGSFTASENHLRHL 60
 DB 41 DSLCPQGYVHSHKNNISICTCKHKGTYLYSDCPSPGPDIVCRECKGTFTASQNYLRQL 100
 QY 61 SCSCKRKGQVEISSCTVDRDTCGCKNQYRHYWSENLFCQFNCSCLNGTVHLSQOE 120
 DB 101 SKCTCRKEMFQVEISPCQADKDTVCCKENQFQYLSETHFQCVDCSPCFNGTVTIIPCKE 160
 QY 121 KQNTVCTCHAGFFLRENECVSCNCKKSLCTKLCPLP 157
 DB 161 TQNTVCNCHAGFFLRESECVFCSHCKKNECKLCLP 197

RESULT 4

GORTT1

tumor necrosis factor receptor 1 precursor - rat
 N:Contains: tumor necrosis factor binding protein 1 (TNF blocking factor)
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 30-Jun-1992 #sequence_revision 07-Oct-1994 #text_change 22-Jun-1999
 C:Accession: B36555
 R:Himmeler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.; Pfizenmaier, K.; Lantz, M.; C
 DNA Cell Biol. 9, 705-715, 1990
 A>Title: Molecular cloning and expression of human and rat tumor necrosis factor receptor
 A:Reference number: A36555; MUID:91090841; PMID:1702293
 A:Accession: B36555
 A:Molecule type: mRNA
 A:Residues: 1-461 <HIM>
 A:Cross-references: GB:M63122; NID:G207361; PIDN:AAA42256.1; PID:G207362
 C:Comment: This protein is one of two known receptors for both TNF-alpha (cachectin) and
 C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
 C:Keywords: duplication; glycoprotein; receptor; transmembrane protein
 F:1-25/Domain: signal sequence #status predicted <SIG>
 F:30-461/Product: tumor necrosis factor receptor type 1 #status predicted <MAT>
 F:30-211/Domain: extracellular #status predicted <EXT>
 F:30-201/Product: tumor necrosis factor binding protein #status predicted <TBP>
 F:44-82/Domain: NGF receptor repeat homology <NG1>
 F:84-126/Domain: NGF receptor repeat homology <NG2>
 F:127-167/Domain: NGF receptor repeat homology <NG3>
 F:168-204/Domain: NGF receptor repeat homology <NG4>
 F:212-234/Domain: transmembrane #status predicted <MEM>
 F:235-461/Domain: intracellular #status predicted <INT>
 F:54,151,201/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 71.1%; Score 669; DB 1; Length 461;
 Best Local Similarity 68.3%; Pred. No. 5.8e-42;
 Matches 110; Conservative 18; Mismatches 33; Indels 0; Gaps 0;

QY 1 DSVCPQGYIHPNNISICTCKHKGTYLYNDPCPGQDTCRECSGSFTASENHLRHL 60
 DB 41 DNLCPQGYIHPNNISICTCKHKGTYLYSDCPSPGQETVCEVCDKGTFTASQNHVROCL 100
 QY 61 SCSCKRKGQVEISSCTVDRDTCGCKNQYRHYWSENLFCQFNCSCLNGTVHLSQOE 120
 DB 101 SKCTCRKEMFQVEISPCQADKDTVCCKENQFQYLSETHFQCVDCSPCFNGTVTIIPCKE 160

QY 121 KQNTVCTCHAGFFLRENECVSCNCKKSLCTKLCPLP 161

DB 161 KQNTVCNCHAGFFLSGNECTPCSHCKKQNECKLCLPPVAN 201

RESULT 5

I34182

tumor necrosis factor receptor 2-related protein - human
 C:Species: Homo sapiens (man)
 C>Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 17-Mar-2000
 C:Accession: I34182
 R:Baens, M.; Chafanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P.
 Genomics 16, 214-218, 1993
 A>Title: Construction and evaluation of a hncDNA library of human 12p transcribed sequenc

C:Comment: This receptor undergoes both N- and O-linked glycosylation.

C:Generics:

A:Gene: GDB:NGFR

A:Cross-references: GDB:120234; OMIM:162010

A:Map position: 17q21-17q22

C:Superfamily: nerve growth factor receptor; NGF receptor repeat homology

C:Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor;

F:1-28/Domain: signal sequence #status predicted <SIG>

F:29-427/Product: nerve growth factor receptor #status experimental <MAT>

F:29-250/Domain: extracellular #status predicted <EXT>

F:32-65/Domain: NGF receptor repeat homology <NG1>

F:67-108/Domain: NGF receptor repeat homology <NG2>

F:109-147/Domain: NGF receptor repeat homology <NG3>

F:149-189/Domain: NGF receptor repeat homology <NG4>

F:197-248/Region: serine/threonine-rich

F:251-272/Domain: transmembrane #status predicted <TM>

F:273-427/Domain: intracellular #status predicted <INT>

F:60/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 19.4%; Score 182.5; DB 1; Length 427;

Best Local Similarity 32.1%; Pred. No. 1.7e-06;

Matches 52; Conservative 25; Mismatches 62; Indels 23; Gaps 11;

QY 4 CPQKTHPPNNNSICCTKCHKGYLYNDCCPGPGDPTDREC-ESGSFTASNNLRLHCLSC 62

Db 32 CPTGLYTH---SGECCKKCNLGEVAGQC-GANQ-TVCEPCLDSVTFSADVATPEKRC 86

QY 63 SKCRKMGQVEISS-CTYDRPTVCGCRKNQYRHWSENLFCQFNLSCLNLT-VHLSQOE 120

Db 87 TEC--VGLQSMASAPCVADADAVCRQ--AVGYODETTGRCACRCVCEAGSLVFSQD 140

QY 121 KONTVC-TCHAGFLRE---NEGVCSNC---KKSLETKR 153

Db 141 KONTVECEPDTGYSDEANHYDPCLPCTVCEPDTERRQLRECR 182

RESULT 7

B38634

tumor necrosis factor receptor type 2 precursor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999

C:Accession: B38634; A40254; S54816

R:Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.T.; Rice, G.C.; Wong, G.H.W.; Chen, E

Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991

A:Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis factor

A:Reference number: A38634; MUID:91187885; PMID:1849278

A:Accession: B38634

A:Molecule type: mRNA

A:Residues: 1-474 <LEW>

A:Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828

R:Goodwin, R.G.; Anderson, D.; Jerry, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jen

Mol. Cell. Biol. 11, 3020-3026, 1991

A:Title: Molecular cloning and expression of the type 1 and type 2 murine receptors for

A:Reference number: A40254; MUID:91246168; PMID:1645445

A:Accession: A40254

A:Molecule type: mRNA

A:Residues: 1-474 <GOO>

A:Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828

R:Kisomernighis, M.; Fellows, R.; Feldmann, M.; Chernajovsky, Y.

Submitted to the EMBL Data Library, May 1995

A:Description: Characterization of the promoter region of the murine p75-TNF receptor.

A:Reference number: S54816

A:Accession: S54816

A:Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-22 <RIS>

A:Cross-references: EMBL:X87128; NID:g809043; PIDN:CAA60618.1; PID:g809044

C:Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology

C:Keywords: cytokine receptor; transmembrane protein

F:1-22/Domain: signal sequence #status predicted <SIG>

F:23-74/Product: tumor necrosis factor receptor type 2 #status predicted <MAT>

F:40-77/Domain: NGF receptor repeat homology <NG1>

F:79-120/Domain: NGF receptor repeat homology <NG2>

Accession: B43692
 Contributor: C. Delange, A.M.; McFadden, G.
 J. Virol. 160, 20-30, 1987
 A:Title: Telomeric poxviruses: Genomic organization and DNA sequence of the telomeric
 A:Reference number: A43692; MUID:87321103; PMID:2820128
 A:Accession: B43692
 A:Status: preliminary
 A:Molecule type: DNA

Db 33 CST

33 CSTGLYTH---SGECCACNLGEGVAQPC-GANQ-TVCEPCLDNVTFSDVVSATEPCXPC 87

A; Cross-references: EMBL:U22579; NID:g623595; PIDN:AAA60933.1; PID:g439102
A; Experimental source: strain Bangladesh 1975
C; Superfamily: myxoma virus T2 protein; NGF receptor repeat homology

Query Match 17.4%; Score 164; DB 2; Length 348;
Best Local Similarity 27.8%; Pred. No. 3.3e-05;
Matches 42; Conservative 17; Mismatches 54; Indels 38; Gaps 8;

Qy	4	CPOQKYIHPONNISICTKCHKGYIYLYNDCPQPODDTCRECSGSTASENHLRHCLSCS	63
Db	31	CKDTEY---KRLNLCLSCSPGYAGRLCDSK-TNTQCTPCSGGTFTSRNNHLPACLSGN	86
Qy	64	-KCKKEMGQVEIISCTVDRTVCGCRKNQVRHYWSENLPQCF-----NSCLINGTVHLS	117
Db	87	GRGNS--NQVETRSCNTHNRICECSPGY-----CILLKGSQGVKACVSTQ----	130

Qy 118 CQEKQNTVCTCHAGFFLRENECVS---CSNC 145
 | : : | | |
Db 131 -----KCGIGYGVSGHTSVGDVICSPC 152

RESULT 15
D36858 gene G4R protein - variola virus
N;Alternate names: B28R protein (COP)
C;Species: variola virus
C;Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text_change 23-Mar-2001
C;Accession: D36858; S46888; S32385; S35987
R;Blinov, V.M.
submitted to GenBank, November 1992
A;Reference number: A36859
A;Accession: D36858
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-349 <BLI>
A;Cross-references: GB:X69198; NID:G456758; PIDN:CAA49137.1; PID:G457087
R;Experimental source: strain India-1967, ssp. major, isolate Ind3
R;Kolyhalov, A.A.; Blinov, V.M.; Gyctorov, V.V.; Pozdnyakov, S.G.; Chizhikov, V.E.; Frolov, I.I.; Kozlov, M.S.; Shchelkunov, S.N.; Sandakhchiev, L.S.; submitted to the EMBL Data Library, April 1992
A;Description: Nucleotide sequence analysis of the region of Variola virus XhoI F O H P
A;Reference number: S46868
A;Accession: S46888
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-349 <COL>
A;Cross-references: EMBL:X67117; NID:g516428; PIDN:CAA47540.1; PID:g516449
R;Experimental source: strain India-1967, isolate Ind3
R;Shchelkunov, S.N.; Blinov, V.M.; Sandakhchiev, L.S.
FEBS Lett. 319, 80-83, 1993
A;Title: Genes of variola and vaccinia viruses necessary to overcome the host protective response
A;Reference number: S32385; PMID:93202281; PMID:8384129

Query Match	17.4%;	Score 164;	DB 2;	Length 349;
Best Local Similarity	27.8%;	Pred. No. 3.3e-05;		
Matches 42;	Conservative 17;	Mismatches 54;	Indels 38;	Gaps 8;

Qy 4 CPOGKYIHPQNNSICCTKCHKGYLYNDCPGPQDTCRECESGSFASENHLRHLCSLCS 63
 : : : : :
Db 32 CKDTEY---KRHNLCCLSCPFGVSRLCDSK-TNTQCTPGSGTTSRNHLPACLSCN 87
 : : : : :
Qy 64 -KCRKEMGOVEISSCTVDRTVCGCRKNQRHYWSENLFQCF-----NCSLCINGTVHLUS 117
 : : : : : : : : : :

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 3, 2002, 14:36:18 ; Search time 13 Seconds
(without alignments)
513.668 Million cell updates/sec

Title: US-09-907-263-2

Perfect score: 941

Sequence: 1 DSVCPQKGYHPQNNISICT.....CSNCKKSLCKLCPQIEN 161

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	941	100.0	455	1	TR1A_HUMAN
2	716.5	76.1	461	1	TR1A_PIG
3	680	72.3	454	1	TR1A_MOUSE
4	674.5	71.7	471	1	TR1A_BOVIN
5	669	71.1	461	1	TR1A_RAT
6	200.5	21.3	176	1	TR23_MOUSE
7	200.5	21.3	176	1	TR12_HUMAN
8	198.5	21.1	180	1	TR22_MOUSE
9	187.5	19.9	435	1	TNR3_HUMAN
10	182.5	19.4	427	1	TR16_HUMAN
11	181.5	19.3	417	1	TR16_MOUSE
12	181	19.2	474	1	TR1B_MOUSE
13	179.5	19.1	326	1	VT2_SFVKA
14	178	18.9	325	1	VT2_SFVKA
15	176.5	18.8	332	1	TNR6_PIG
16	176.5	18.8	425	1	TR16_RAT
17	167.5	17.8	289	1	TNR5_MOUSE
18	167.5	17.8	415	1	TNR3_MOUSE
19	167	17.7	269	1	TNR5_BOVIN
20	166.5	17.7	323	1	TNR6_BOVIN
21	166.5	17.7	323	1	CRMB_CAMPS
22	164	17.4	349	1	CRMB_VARY
23	164	17.4	351	1	CRMB_COMPX
24	164	17.4	401	1	T11B_HUMAN
25	162.5	17.3	327	1	TNR6_MOUSE
26	161	17.1	461	1	TR1B_HUMAN
27	158	16.8	401	1	T11B_RAT
28	154	16.4	401	1	T11B_MOUSE
29	147	15.6	324	1	TNR6_RAT
30	145	15.4	416	1	TR16_CHICK
31	142	15.1	283	1	TR14_HUMAN
32	142	15.1	386	1	T10D_HUMAN
33	141	15.0	1680	1	FUR2_DROME

ALIGNMENTS

RESULT 1

ID	TR1A_HUMAN	STANDARD;	PRT;	455 AA.
AC	P19438;			
DT	01-FEB-1991 (Rel. 17, Created)			
DT	01-FEB-1991 (Rel. 17, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Tumor necrosis factor receptor superfamily member 1A precursor (p60)			
DE	(TNF-R1) (TNF-RI) (p55) (CD120a) [Contains: Tumor necrosis factor			
DE	binding protein 1 (TFPI)]			
GN	TNFRSF1A OR TNFR1 OR TNFR.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]_SEQUENCE FROM N.A.			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Placenta;			
RX	MEDLINE=90235285; PubMed=2158863;			
RA	Schall T.J., Lewis M., Koller K.J., Lee A., Rice G.C., Wong G.H.W.,			
RA	Getanaga T., Granger G.A., Lentz R., Raab H., Kohr W.J., Goeddel D.V.,			
RT	"Molecular cloning and expression of a receptor for human tumor			
RT	necrosis factor.";			
RL	Cell 61:361-370(1990).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=90235284; PubMed=2158862;			
RA	Loetscher H., Pan Y.-C.E., Lahm H.-W., Gentz R., Brockhaus M.,			
RA	Tabuchi H., Lesslauer W.,			
RT	"Molecular cloning and expression of the human 55 kd tumor necrosis			
RT	factor receptor.";			
RL	Cell 61:351-359(1990).			
RN	[3]			
RP	SEQUENCE FROM N.A. AND SEQUENCE OF 41-53; 110-124 AND 199-201.			
RX	MEDLINE=91090621; PubMed=1698610;			
RA	Nophar Y., Kemper O., Brakebusch C., Engelmann H., Zwang R.,			
RA	Aderka D., Holtmann H., Wallach D.;			
RT	"Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA			
RT	for the type I TNF-R, cloned using amino acid sequence data of its			
RT	soluble form, encodes both the cell surface and a soluble form of the			
RT	receptor.";			
RL	EMBO J. 9:3269-3278(1990).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=91090841; PubMed=1702293;			
RA	Himmeler A., Maurer-Fogy I., Kroenke M., Scheurich P., Pfizenmaier K.,			
RA	Lantz M., Olsson I., Hauptmann R., Stratowa C., Adolf G.R.;			
RT	"Molecular cloning and expression of human and rat tumor necrosis			
RT	factor receptor chain (p60) and its soluble derivative, tumor			
RT	necrosis factor-binding protein.";			
RL	DNA Cell Biol. 9:705-715(1990).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Placenta;			
RX	MEDLINE=91017509; PubMed=2170974;			
RA	Gray P.W., Barrett K., Chantry D., Turner M., Feldman M.;			

P41272 mus musculus
P25942 homo sapien
O14798 h tumor nec
P26842 homo sapien
O14763 homo sapien
Q9nj15 branchioeco
Q04592 mus musculus
P92127 giardia lam
Q9epu5 mus musculus
Q92824 homo sapien
P47741 mus musculus
P25445 homo sapien

34 139.5 14.8 250 1 TNR7_MOUSE
35 139.5 14.8 277 1 TNR5_HUMAN
36 139.5 14.8 259 1 T10C_HUMAN
37 138.5 14.7 260 1 TNR7_HUMAN
38 137 14.6 440 1 T10B_HUMAN
39 134 14.2 1696 1 PKK5_BRACL
40 134 14.2 1877 1 PKK5_MOUSE
41 133 14.1 687 1 VS41_GIALA
42 132.5 14.1 655 1 TR21_MOUSE
43 132 14.0 913 1 PKK5_HUMAN
44 131.5 14.0 272 1 TNR4_MOUSE
45 130.5 13.9 335 1 TNR6_HUMAN

RT "Cloning of human tumor necrosis factor (TNF) receptor cDNA and
 RT expression of recombinant soluble TNF-binding protein.",
 RL Proc. Natl. Acad. Sci. U.S.A. 87:7380-7384(1990).
 RN [6]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92250049; PubMed=1315717;
 RA Fuchs P., Strehl S., Dworzak M., Himmeler A., Ambros P.F.;
 RT "Structure of the human TNF receptor 1 (p60) gene (TNFR1) and
 RT localization to chromosome 12p13.",
 RL Genomics 13:219-224(1992).
 RN [7]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Muscle;
 RA Strausberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RN [8]
 RP SEQUENCE OF 41-45.
 RX MEDLINE=90110215; PubMed=2153136;
 RA Engelmann H., Novick D., Wallach D.;
 RT "Two tumor necrosis factor-binding proteins purified from human
 RT urine. Evidence for immunological cross-reactivity with cell surface
 RT tumor necrosis factor receptors.",
 RL J. Biol. Chem. 265:11531-1536(1990).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.85 ANGSTROMS) OF 30-211 IN COMPLEX WITH TNFB.
 RX MEDLINE=93258809; PubMed=8387891;
 RA Banner D.W., D'Arcy A., Janes W., Genz R., Schoenfeld H.-J.,
 RT "Crystal structure of the soluble human 55 kd TNF receptor-human TNF
 RT beta complex: implications for TNF receptor activation.",
 RL Cell 73:431-445(1993).
 RN [10]
 RP X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 41-202.
 RX MEDLINE=97094982; PubMed=8939750;
 RA Naismith J.H., Devine T.Q., Khoro H., Sprang S.R.;
 RT "Structures of the extracellular domain of the type I tumor necrosis
 RT factor receptor.",
 RL Structure 4:1251-1262(1996).
 RN [11]
 RP VARIANTS FHF ARG-59; TYR-62; MET-79; PHE-81; ARG-117 AND TYR-117.
 RX MEDLINE=99213501; PubMed=10199409;
 RA McDermott M.F., Aksentjevich I., Galon J., McDermott E.M.,
 RA Ogunkolade B.W., Centola M., Mansfield E., Gadiña M., Karenko L.,
 RA Petersen T., McCarthy J., Frucht D.M., Aringer M., Terosyan Y.,
 RA Teppo A.-M., Wilson M., Karaarslan H.M., Wan Y., Todd I., Wood G.,
 RA Schlienger R., Kumarajewa T.R., Cooper S.M., Vella J.P., Amos C.I.,
 RA Mulley J., Quane K.A., Molloy M.G., Rnaki A., Powell R.J.,
 RA Hiltman G.A., O'Shea J., Kastner D.L.;
 RT "Germline mutations in the extracellular domains of the 55 kDa TNF
 RT receptor, TNFR1, define a family of dominantly inherited
 RT autoinflammatory syndromes.",
 RL Cell 97:133-144(1999).
 CC -1- FUNCTION: Receptor for TNFRSF2/TNF-alpha and homotrimeric
 CC TNFRSF1/lymphotoxin-alpha. The adaptor molecule FADD recruits
 CC caspase-8 to the activated receptor. The resulting death-inducing
 CC signaling complex (DISC) performs caspase-8 proteolytic activation
 CC which initiates the subsequent cascade of caspases (aspartate-
 CC specific cysteine proteases) mediating apoptosis. Contributes to
 CC the induction of noncytotoxic TNF effects including anti-viral
 CC state and activation of the acid sphingomyelinase.
 CC -1- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
 CC HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
 CC PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
 CC WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
 CC PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO
 CC TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
 CC ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
 CC NF-KAPPA B SIGNALING.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein and secreted.
 CC -1- DOMAIN: THE DOMAIN THAT INDUCES A-SMASE IS PROBABLY IDENTICAL TO
 CC THE DEATH DOMAIN. THE N-SMASE ACTIVATION DOMAIN (NSD) IS BOTH
 CC NECESSARY AND SUFFICIENT FOR ACTIVATION OF N-SMASE.
 CC -1- PTM: The soluble form is produced from the membrane form by

CC proteolytic processing.
 CC -1- DISEASE: Defects in TNFRSF1A are a cause of autosomal dominant
 CC familial hibernian fever (FHF), a disease characterized by
 CC recurrent fever, abdominal pain, localized tender skin lesions and
 CC myalgia.
 CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
 CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
 CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD120a entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd120a.htm".
 CC -----
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 CC EMBL; X55313; CA339021.1; -;
 CC EMBL; M33294; AAA03210.1; -;
 CC EMBL; M58286; AAA36753.1; -;
 CC EMBL; M63121; AAA36754.1; -;
 CC EMBL; M75866; AAA61201.1; -;
 CC EMBL; M75864; AAA61201.1; -;
 CC EMBL; M75865; AAA61201.1; JOINED.
 CC EMBL; M60765; AAA36756.1; -;
 CC EMBL; A21522; CA01558.1; -;
 CC EMBL; BC010140; AAH10140.1; -;
 CC PIR; A34899; G0HUT1.
 CC PIR; A35010; A35010.
 CC PIR; S12057; S12057.
 CC PIR; A38208; A38208.
 CC PDB; 1TNR; 31-JUL-94.
 CC PDB; 1NCF; 07-DEC-95.
 CC PDB; 1EXT; 11-JAN-97.
 CC GeneW; HGNC:11916; TNFRSF1A.
 CC MIM; 191180; -;
 CC MIM; 142680; -;
 CC InterPro; IPR000488; Death.
 CC InterPro; IPR001368; TNFR_c6.
 CC Pfam; PF00020; TNFR_c6; 4.
 CC Pfam; PF00531; death; 1.
 CC ProDom; PD000771; TNFR_c6; 1.
 CC SMART; SM00005; DEATH; 1.
 CC SMART; SM00208; TNFR; 4.
 CC PROSITE; PS00652; TNFR_NGFR_1; 3.
 CC PROSITE; PS00500; TNFR_NGFR_2; 3.
 CC PROSITE; PS00017; DEATH_DOMAIN; 1.
 CC Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal;
 CC Disease mutation; Polymorphism; 3D-structure.
 CC FT CHAIN 1 21
 CC FT SIGNAL 1 21
 CC FT 22 455
 CC FT 21
 CC CHAIN 41 291
 CC FT DOMAIN 22 211
 CC FT TRANSMEM 212 234
 CC FT DOMAIN 235 455
 CC FT REPEAT 43 82
 CC FT REPEAT 83 125
 CC FT REPEAT 126 166
 CC FT REPEAT 167 196
 CC FT DOMAIN 338 348
 CC FT DOMAIN 356 441
 CC FT DOMAIN 44 58
 CC FT DISULFID 59 72
 CC FT DISULFID 62 81
 CC FT DISULFID 84 99
 CC FT DISULFID 102 117
 CC FT DISULFID 105 125
 CC FT DISULFID 127 143
 CC FT DISULFID 146 158
 CC FT DISULFID 149 166
 CC FT DISULFID 168 179
 CC TUMOR NECROSIS FACTOR RECEPTOR
 CC SUPERFAMILY MEMBER 1A, MEMBRANE FORM.
 CC TUMOR NECROSIS FACTOR BINDING PROTEIN 1.
 CC EXTRACELLULAR (POTENTIAL).
 CC POTENTIAL.
 CC CYTOPLASMIC (POTENTIAL).
 CC TNFR-CYS 1.
 CC TNFR-CYS 2.
 CC TNFR-CYS 3.
 CC TNFR-CYS 4.
 CC N-SMASE ACTIVATION DOMAIN (NSD).
 CC DEATH.

Query Match 100.0%; Score 941; DB 1; Length 455;
 Best Local Similarity 100.0%; Pred. No. 1.2e-71;
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVCPQGYIHPQNNISCTCKHKGTYLYNDPCPGQDTDCRECSGFTASENHLRCL 60
 DB 41 DSVCPQGYIHPQNNISCTCKHKGTYLYNDPCPGQDTDCRECSGFTASENHLRCL 100

QY 61 SCSKCKEMQVEISSCTVDRDTCGCRKNQVRYHWSNLFQCFNCSLCNGTVHLSQOE 120
 DB 101 SCSKCKEMQVEISSCTVDRDTCGCRKNQVRYHWSNLFQCFNCSLCNGTVHLSQOE 160

QY 121 KONTVCTCHAGFFLRENECVSCNCKSLECTKLCPLQIEN 161
 DB 161 KONTVCTCHAGFFLRENECVSCNCKSLECTKLCPLQIEN 201

RESULT 2

TRIA_PIG
 ID TRIA_PIG STANDARD; PRT; 461 AA.
 AC P50555;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 1A precursor (p60)
 DE (TNF-R1) (TNF-R1) (p55).
 GN TNFRSF1A OR TNFR1.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 EX MEDLINE=96011645; PubMed=7590278;
 RA Suter B., Pauli U.H.;
 RT "Cloning of the cDNA encoding the porcine p55 tumor necrosis factor receptor.";
 RL Gene 163:263-266(1995).

CC -!- FUNCTION: Receptor for TNFSP2/TNF-alpha and homotrimeric TNFSP1/lymphotoxin-alpha. The adaptor molecule FADD recruits signaling-8 to the activated receptor. The resulting death-inducing signaling complex (DISC) performs caspase-8 proteolytic activation which initiates the subsequent cascade of caspases (aspartate-specific cysteine proteases) mediating apoptosis (By similarity).
 CC -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND NF-KAPPA B SIGNALING (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
 CC -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.

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 CC -----
 CC EMBL; U19994; AAC48499.1; -;
 CC HSSP; P19438; 1TNF.
 CC InterPro; IPR000488; Death.
 CC InterPro; IPR001368; TNFR.c6.
 CC Pfam; PF00020; TNFR_c6; 3.
 CC Pfam; PF00531; death; 1.
 CC ProDom; PD000771; TNFR_c6; 1.

DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00208; TNFR; 3.
 DR PROSITE; PS00552; TNFR_NGFR_1; 3.
 DR PROSITE; PS00550; TNFR_NGFR_2; 2.
 DR PROSITE; PS0017; DEATH_DOMAIN; 1.
 KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
 FT SIGNAL 1 21 POTENTIAL.
 FT CHAIN 22 461 TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 1A. EXTRACELLULAR (POTENTIAL). POTENTIAL.
 FT DOMAIN 22 210 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 211 233 TNFR-CYS 1.
 FT REPEAT 234 461 TNFR-CYS 2.
 FT REPEAT 83 125 TNFR-CYS 3.
 FT REPEAT 126 166 TNFR-CYS 4.
 FT REPEAT 167 195 N-SMASE ACTIVATION DOMAIN (NSD).
 FT DOMAIN 340 350 DEATH.
 FT DOMAIN 362 447 BY SIMILARITY.
 FT DISULFID 44 58 BY SIMILARITY.
 FT DISULFID 59 72 BY SIMILARITY.
 FT DISULFID 62 81 BY SIMILARITY.
 FT DISULFID 84 99 BY SIMILARITY.
 FT DISULFID 102 117 BY SIMILARITY.
 FT DISULFID 105 125 BY SIMILARITY.
 FT DISULFID 127 143 BY SIMILARITY.
 FT DISULFID 146 158 BY SIMILARITY.
 FT DISULFID 149 166 BY SIMILARITY.
 FT DISULFID 168 179 BY SIMILARITY.
 FT DISULFID 182 194 BY SIMILARITY.
 FT DISULFID 185 190 BY SIMILARITY.
 FT CARBOHYD 54 54 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 86 86 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 145 145 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 151 151 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 461 AA; 50696 MW; CD72361EC60C9D43 CRC64;

Query Match 76.1%; Score 716.5; DB 1; Length 461;
 Best Local Similarity 77.4%; Pred. No. 5.8e-53;
 Matches 120; Conservative 12; Mismatches 22; Indels 1; Gaps 1;

QY 1 DSVCPQGYIHPQNNISCTCKHKGTYLYNDPCPGQDTDCRECSGFTASENHLRCL 60
 DB 41 ESLCPQGYIHPQNNISCTCKHKGTYLYNDPCPGQDTDCRECSGFTASENHLRCL 100

QY 61 SCSKCKEMQVEISSCTVDRDTCGCRKNQVRYHWSNLFQCFNCSLCNGTVHLSQOE 120
 DB 101 SCSKCKEMQVEISSCTVDRDTCGCRKNQVRYHWSNLFQCFNCSLCNGTVHLSQOE 160

QY 121 KONTVCTCHAGFFLRENECVSCNCKSLECTKLC 155
 DB 161 KQDTICNCHSGFFLRDKCEVCVCKNA-DCKNLC 194

RESULT 3

TRIA_MOUSE
 ID TRIA_MOUSE STANDARD; PRT; 454 AA.
 AC P25118;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 1A precursor (p60)
 DE (TNF-R1) (TNF-R1) (p55).
 GN TNFRSF1A OR TNFR1 OR TNFR-1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91187885; PubMed=1849278;
 RA Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C.,
 RA Wong G.H., Chen E.Y., Goeddel D.V.;
 RT "Cloning and expression of cDNAs for two distinct murine tumor

RT necrosis factor receptors demonstrate one receptor is species specific.";
 RT Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834 (1991).
 RL (2)
 RN SEQUENCE FROM N.A.
 RX MEDLINE=91246168; PubMed=1645445;
 RA Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I.,
 RA Copeland N.G., Jenkins N.A., Smith C.A.;
 RT "Molecular cloning and expression of the type 1 and type 2 murine
 RT receptors for tumor necrosis factor.";
 RL Mol. Cell. Biol. 11:3020-3026 (1991).
 RN (3)
 RN SEQUENCE FROM N.A.
 RX MEDLINE=91285014; PubMed=1647956;
 RA Barrett K., Taylor-Fishwick D.A., Cope A.P., Klesonerghis A.M.,
 RA Gray P.W., Fellmann M., Foxwell B.M.J.;
 RT "Cloning, expression and cross-linking analysis of the murine p55
 RT tumor necrosis factor receptor.";
 RL Eur. J. Immunol. 21:1649-1656 (1991).
 RN (4)
 RN SEQUENCE FROM N.A.
 RC TISSUE=SpLeen;
 RX MEDLINE=92039815; PubMed=1657766;
 RA Rothe J.G., Brockhaus M., Gentz R., Lesslauer W.;
 RT "Molecular cloning and expression of the mouse Tnf receptor type b.";
 RL Immunogenetics 34:338-340 (1991).
 RN (5)
 RN SEQUENCE FROM N.A.
 RX MEDLINE=94245292; PubMed=8188324;
 RA Bebo B.F., Linthicum D.S.;
 RT "Nucleotide sequence of the TNF type I receptor from a mouse
 RT endothelioma cell line.";
 RL Immunogenetics 39:450-451 (1994).
 RN (6)
 RN SEQUENCE FROM N.A.
 RX MEDLINE=93156721; PubMed=8381516;
 RA Rothe J., Bluetmann H., Gentz R., Lesslauer W., Steinmetz M.;
 RT "Genomic organization and promoter function of the murine tumor
 RT necrosis factor receptor beta gene.";
 RL Mol. Immunol. 30:165-175 (1993).
 RN (7)
 RN SEQUENCE FROM N.A.
 RA Strauberg R.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric
 CC TNFSF1/lymphotoxin-alpha. The adaptor molecule FADD recruits
 CC signaling complex (DISC) performs caspase-8 proteolytic activation
 CC which initiates the subsequent cascade of caspases (aspartate-
 CC specific cysteine proteases) mediating apoptosis (By similarity).
 CC -1- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
 CC HOMODIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
 CC PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
 CC WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
 CC PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO
 CC TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
 CC ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
 CC NF-KAPPA B SIGNALING (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
 CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
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 CC
 CC EMBL; M50468; AAA39751.1; -;
 DR EMBL; M59377; AAA40464.1; -;
 DR EMBL; X59238; CAA41922.1; -;

DR EMBL; X57796; CAA40936.1; -;
 DR EMBL; L26349; AAA59361.1; -;
 DR EMBL; M76656; AAA40465.1; -;
 DR EMBL; M88067; AAA40465.1; JOINED.
 DR EMBL; M76655; AAA40465.1; JOINED.
 DR EMBL; BC004599; AAH04599.1; -;
 DR PIR; A38634; GQMSTL.
 DR PIR; S16677; S16677.
 DR PIR; S19021; S19021.
 DR HSSP; P19438; IEXT.
 DR MGD; MGI:1314884; Tnfalfa.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR001368; TNFR_c6.
 DR Pfam; PF00020; TNFR_c6; 4.
 DR Pfam; PF00531; death; 1.
 DR ProDom; PD000771; TNFR_c6; 1.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00208; TNFR; 3.
 DR PROSITE; PS00652; TNFR_NGFR_1; 3.
 DR PROSITE; PS50050; TNFR_NGFR_2; 3.
 DR PROSITE; PS50017; DEATH_DOMAIN; 1.
 DR Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
 FT SIGNAL 1 21
 FT CHAIN 22 454
 FT
 FT DOMAIN 22 212
 FT TRANSMEM 213 235
 FT DOMAIN 236 454
 FT REPEAT 43 82
 FT REPEAT 83 125
 FT REPEAT 126 166
 FT REPEAT 167 196
 FT DOMAIN 339 349
 FT DOMAIN 356 441
 FT DISULFID 44 58
 FT DISULFID 59 72
 FT DISULFID 62 81
 FT DISULFID 84 99
 FT DISULFID 102 117
 FT DISULFID 105 125
 FT DISULFID 127 143
 FT DISULFID 146 158
 FT DISULFID 149 166
 FT DISULFID 168 179
 FT DISULFID 182 195
 FT DISULFID 185 191
 FT CARBOHYD 54
 FT CARBOHYD 151 151
 FT CARBOHYD 202 202
 FT CONFLICT 394 394
 SQ SEQUENCE 454 AA; 50129 MW; 0710C2E8C3C2B6D9 CRC64;
 Query Match 72.3%; Score 680; DB 1; Length 454;
 Best Local Similarity 71.3%; Pred. No. 6,2e-50;
 Matches 112; Conservative 19; Mismatches 26; Indels 0; Gaps 0;
 QY 1 DSVCPQGVYHPPNNSICCTCKHKTGYLYNDCPGQDTCREESGFSFASENHLRHCL 60
 DB 41 DDLCPGVKSHKNSICTCKHKTGYLYSDCPGPRDTCRECEKGTFTASQVLYRCL 100
 QY 61 SCSKRKEGVETSSCTVDBDTCGCRKNQYHWSNNLFCQNCNCLNGTHTLSOE 120
 DB 101 SKTKRKEGVETSSCPADKDTVCCKENPQRLSTHFQCVDCSPFNGVTYIPCKE 160
 QY 121 KONTVCTCHAGFLRENECVSCNCKSLCTKTLCLP 157
 DB 161 TONTVONCHAGFLRESECVPSHCKNEBCKLCLP 197
 RESULT 4
 TRIA BOVIN
 ID TRIA BOVIN
 AC 019131;
 STANDARD; PRT; 471 AA.

DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 1A precursor (p60)
 DE (TNF-R1) (TNF-R1) (p55).
 GN TNFRSF1A OR TNFR1.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]_TaxID=9913;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Aorta;
 RX MEDLINE=98273505; PubMed=9613449;
 RA Lee E.-K., Kehrl M.E. Jr., Taylor M.J.;
 RT "Cloning and sequencing of cDNA encoding bovine tumor necrosis factor
 (TNF)-receptor 1";
 RL Vet. Immunol. Immunopathol. 61:379-385(1998).
 CC -!- FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric
 CC TNFSF1/lymphotoxin-alpha. The adaptor molecule FADD recruits
 CC caspase-8 to the activated receptor. The resulting death-inducing
 CC signaling complex (DISC) performs caspase-8 proteolytic activation
 CC which initiates the subsequent cascade of caspases (aspartate-
 CC specific cysteine proteases) mediating apoptosis (By similarity).
 CC -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
 CC HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
 CC PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
 CC WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
 CC PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO
 CC TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
 CC ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
 CC NF-KAPPA B SIGNALING (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type 1 membrane protein.
 CC -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
 CC -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
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 CC
 CC -----
 CC EMBL; U0937; AAB65143.1; -;
 CC HSP; P19438; 1TNF;
 CC InterPro; IPR000488; Death.
 CC InterPro; IPR001368; TNFR_c6.
 CC Pfam; PF00020; TNFR_c6; 3.
 CC Pfam; PF00531; death; 1.
 CC ProDom; PD000771; TNFR_c6; 1.
 CC SMART; SM00005; DEATH; 1.
 CC SMART; SM00208; TNFR; 3.
 CC PROSITE; PS00652; TNFR_NGFR_1; 3.
 CC PROSITE; PS00050; TNFR_NGFR_2; 3.
 CC PROSITE; PS00017; DEATH DOMAIN; 1.
 CC Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
 KW SIGNAL 1 21 POTENTIAL.
 FT CHAIN 22 471 TUMOR NECROSIS FACTOR RECEPTOR
 FT SUPERFAMILY MEMBER 1A.
 FT EXTRACELLULAR (POTENTIAL).
 FT POTENTIAL.
 FT CYTOPLASMIC (POTENTIAL).
 FT TNFR-CYS 1.
 FT TNFR-CYS 2.
 FT TNFR-CYS 3.
 FT TNFR-CYS 4.
 FT N-SMASE ACTIVATION DOMAIN (NSD).
 FT DEATH.
 FT BY SIMILARITY.
 FT BY SIMILARITY.
 FT BY SIMILARITY.
 FT BY SIMILARITY.

FT DISULFID 84 99 BY SIMILARITY.
 FT DISULFID 102 117 BY SIMILARITY.
 FT DISULFID 105 125 BY SIMILARITY.
 FT DISULFID 127 143 BY SIMILARITY.
 FT DISULFID 146 158 BY SIMILARITY.
 FT DISULFID 149 166 BY SIMILARITY.
 FT DISULFID 168 179 BY SIMILARITY.
 FT DISULFID 182 194 BY SIMILARITY.
 FT DISULFID 185 190 BY SIMILARITY.
 FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 145 145 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 471 AA; 51367 MW; 5243EP514DFE81C4 CRC64;
 Query Match 71.7%; Score 674.5; DB 1; Length 471;
 Best Local Similarity 71.6%; Pred. No. 1.8e-49;
 Matches 111; Conservative 17; Mismatches 26; Indels 1; Gaps 1;
 QY 1 DSVCPQGYTHPONNSICTCTCKHKGTYLYNDPCPGQDTCDCRECSGSFTASENHLRCL 60
 DB 41 ESPCPQGYNHPPONNSICTCTCKHKGTYLYNDPCPGDTCDCVCAPTGTALENHURCL 100
 QY 61 SCCKRREMGOVEISSCTVDRTVCCCRKNQVRYHWSNLFCQFNCSLCLNGTVHLSQCE 120
 DB 101 SCGRCDENFQVEISPCWVDRDTCVCCRNQVRYWGETGFRCLNCSLCPNGTVNIPCE 160
 QY 121 KQNTVCTCHAGFPILRENECVSCNCKKSECTKLC 155
 DB 161 RQDTICHGMGFFLGKAGKICSDCKNK-ECEKLC 194
 RESULT 5
 TRIA-RAT
 ID TRIA-RAT STANDARD; PRT; 461 AA.
 AC P22934; Q91V30; Q91Y93;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 1A precursor (p60)
 DE (TNF-R1) (TNF-R1) (p55).
 GN TNFRSF1A OR TNFR1 OR TNFR-1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91090841; PubMed=1702293;
 RA Himmler A., Maurer-Pogoy I., Kroenke M., Scheurich P., Pfizenmaier K.,
 RA Lantzer M., Olsson I., Hauptmann R., Stratowa C., Adolf G.R.;
 RT "Molecular cloning and expression of human and rat tumor necrosis
 RT factor receptor chain (p60) and its soluble derivative, tumor
 RT necrosis factor-binding protein.";
 RL DNA Cell Biol. 9:705-715(1990).
 RN [2]
 RP SEQUENCE FROM N.A., AND VARIANTS VAL-230 AND PRO-295.
 RC STRAIN=Various;
 RA Furuya T., Saistrom J.L., Bina J., Hashimoto A., Dobbins D.E.,
 RA Wilder R.L., Remmers E.F.;
 RT "Polymorphisms of the tumor necrosis factor receptor type 1 locus
 RT among autoimmune susceptible and resistant inbred rat strains.";
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric
 CC TNFSF1/lymphotoxin-alpha. The adaptor molecule FADD recruits
 CC caspase-8 to the activated receptor. The resulting death-inducing
 CC signaling complex (DISC) performs caspase-8 proteolytic activation
 CC which initiates the subsequent cascade of caspases (aspartate-
 CC specific cysteine proteases) mediating apoptosis (By similarity).
 CC -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
 CC HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
 CC PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
 CC WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
 CC PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO

CC	TNFR1.COMPLEX BY THEIR ASSOCIATION WITH TRADD, THIS COMPLEX
CC	ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC	NE-KAPPA B SIGNALING (BY SIMILARITY).
CC	-1- SUBCELLULAR LOCATION: Type 1 membrane protein.
CC	-1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC	-1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC	-----
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CC	or send an email to license@isb-sib.ch).
CC	-----
CC	EMBL; M63122; AAA42256.1; -
DR	EMBL; AF329976; AAK53562.1; -
DR	EMBL; AF329977; AAK53563.1; -
DR	EMBL; AF329981; AAK53567.1; -
DR	EMBL; AF329978; AAK53564.1; -
DR	EMBL; AF329979; AAK53565.1; -
DR	EMBL; AF329980; AAK53566.1; -
DR	PIR; B36555; B36555.
DR	HSSP; P19438; INCF.
DR	InterPro; IPR000468; Death.
DR	InterPro; IPR001368; TNFR_C6.
DR	Pfam; PF00020; TNFR_C6; 4.
DR	Pfam; PF00531; Death; 1.
DR	ProDom; PD000771; TNFR_C6; 1.
DR	SMART; SMO0208; TNFR; 3.
DR	PROSITE; PS00652; TNFR_NGFR_1; 3.
DR	PROSITE; PS00650; TNFR_NGFR_2; 3.
DR	PROSITE; PS50017; DEATH_DOMAIN; 1.
DR	Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
KW	SIGNAL
FT	CHAIN 1 21
FT	22 461
FT	DOMAIN 22 211
FT	TRANSMEM 212 234
FT	DOMAIN 235 461
FT	REPEAT 43 82
FT	REPEAT 83 125
FT	REPEAT 126 166
FT	REPEAT 167 196
FT	DOMAIN 344 354
FT	DOMAIN 363 448
FT	DISULFID 44 58
FT	DISULFID 59 72
FT	DISULFID 62 81
FT	DISULFID 84 99
FT	DISULFID 102 117
FT	DISULFID 105 125
FT	DISULFID 127 143
FT	DISULFID 146 158
FT	DISULFID 149 166
FT	DISULFID 168 179
FT	DISULFID 182 195
FT	DISULFID 185 191
FT	CARBOHYD 54 54
FT	CARBOHYD 151 151
FT	CARBOHYD 201 201
FT	VARIANT 230 230
FT	VARIANT 295 295
FT	SEQUENCE 461 AA; 50969 MW; 59696 MW;
FT	Query Match 71.1%; Score 669; DB 1; Length 461;
FT	Best Local Similarity 68.3%; Pred. No. 5,2e-49;
FT	Matches 110; Conservative 18; Mismatches 33; Indels 0; Gaps 0;
QY	1 DSVCGGKGIHHQNNNSICTCKCHKIGYLVINDCGPGPDIDTCRCESGSPFASENHLRHCL 60

D6		41	DNLBPQKXIAHPKKNNSICCTCKCHKGTILVSDPCSPGGETICEVDKGTFLPNSOHVAQCCL	100
QY		61	SCSKCRKEMGOVEIISCTVDRAITVCGRKNOYRHYWSENLFQCFNCGLCLINGTVHLSQCE	120
D6		101	SCKTCRKEMFQVEISPCAKMDVTGCGKKNOFYUILLSETHQCVDCSPFCNGTATIPCKE	160
QY		121	KONTVCTCHAGFFLRENECVCSGCNCKSLSBETKTLCLQIQEN	161
D6		161	KONTVCNCHAGFFLSGNECTPCHCKKNQECMKLCPLPVAN	201
RESULT	6			
TR23_MOUSE				
ID	TR23_MOUSE	STANDARD;	PRT;	176 AA.
AC	Q9ER63; Q8VHC0;			
DT	15-JUN-2002 (Rel. 41, Created)			
DT	15-JUN-2002 (Rel. 41, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, last annotation update)			
DE	Tumor necrosis factor receptor superfamily member 23 (Tumor necrosis factor receptor p60 homolog 1) (TNF receptor family member SOB).			
GN	TNFRSF23 OR TNFRSF11 OR TNFRF11.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
CX	NCBI_TaxID=10090;			
RN	(1)			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=129/SV; TISSUE=Embryonic stem cells;			
RX	MEDLINE=20519229; PubMed=11063728;			
RA	Emmelsen S., Stroedicke M., Paulsen M., Franck O., Reinhardt R.,			
RA	Lane N., Reik W., Walter J.			
RT	"Sequence and functional comparison in the Beckwith-Wiedemann region:			
RT	implications for a novel imprinting centre and extended imprinting.";			
RL	Hum. Mol. Genet. 9:2691-2706(2000).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Pan G., Mao W., Risser P.			
RT	"Characterization of SOB, a member of the TNFR family."			
RL	Submitted (JUL-2001) to the EMBL/Genbank/DDBJ databases.			
CC	-1- SUBCELLULAR LOCATION: Type II membrane protein (Potential).			
CC	-1- TISSUE SPECIFICITY: Ubiquitous.			
CC	-1- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; AJ278264; CAC16405.1; -			
DR	EMBL; AJ276505; CAC27352.1; -			
DR	EMBL; AY046550; AAL05072.1; -			
DR	HSSP; P19438; TEXT.			
DR	MGI; MGI:1930269; Thfrsf23.			
DR	InterPro; IPR001368; TNFR_C6.			
DR	PIfam; PF00020; TNFR_C6; 3.			
DR	SMART; SM0208; TNFR_3.			
DR	PROSITE; PS50050; TNFR_NGRF_2; 2.			
KW	Receptor; Signal-anchor; Transmembrane; Glycoprotein; Repeat.			
FT	DOMAIN	1	9	
FT	TRANSMEM	10	30	
FT				
FT	DOMAIN	31	176	
FT	REPEAT	37	72	
FT	REPEAT	74	114	
FT	REPEAT	115	155	
FT	DISULFID	38	49	
FT	DISULFID	50	63	
FT	DISULFID	53	72	
FT	DISULFID	75	90	


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FT CHAIN 31 435 TUMOR NECROSIS FACTOR RECEPTOR
FT 31 227 SUPERFAMILY MEMBER 3.
FT DOMAIN 228 248 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 249 435 POTENTIAL.
FT 249 435 CYTOPLASMIC (POTENTIAL).
FT REPEAT 42 81 TNFR-CYS 1.
FT REPEAT 82 124 TNFR-CYS 2.
FT REPEAT 125 168 TNFR-CYS 3.
FT REPEAT 169 211 TNFR-CYS 4.
FT DISULFID 43 58 BY SIMILARITY.
FT DISULFID 59 72 BY SIMILARITY.
FT DISULFID 62 80 BY SIMILARITY.
FT DISULFID 83 98 BY SIMILARITY.
FT DISULFID 101 116 BY SIMILARITY.
FT DISULFID 104 124 BY SIMILARITY.
FT DISULFID 126 132 BY SIMILARITY.
FT DISULFID 139 148 BY SIMILARITY.
FT DISULFID 142 167 BY SIMILARITY.
FT DISULFID 170 185 BY SIMILARITY.
FT CARBOHYD 40 40 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 435 AA; 46709 MW; 624626B6022F656F CRC64;

Query Match 19.9%; Score 187.5; DB 1; Length 435;
Best Local Similarity 32.7%; Pred. No. 6.2e-09;
Matches 49; Conservative 17; Mismatches 71; Indels 13; Gaps 7;

QY 8 KYIHPONNSICCTCHKGYLYNDCCPGQDTCRECESSGFASSENHLRHCLSCSKCRK 67
DB 49 EYEBQHR-ICCSRCPRGTYSAC-SRIDTYCATANSYEHNNYLLTQLCRPCDP 106
QY 68 EMGVEISSCTVDRTVCGCRKNQYRHYSENLFQCFNCSL---CLNGVHLSQD--KQ 122
DB 107 VMGIEELAPCTSKKTKCQCPGFCAMA---LECHCELLSDCPGTEALDKDVGKG 163
QY 123 NTVCT-CHAGFFLRENECVSCNCKSLC 151
DB 164 NNHCVPCKAGHF--QNTSSPSARCQPHTRC 191

RESULT 10
TR16_HUMAN STANDARD; PRT; 427 AA.
ID TR16_HUMAN STANDARD; PRT; 427 AA.
AC P08138;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 16 precursor (low-
DE affinity nerve growth factor receptor) (NGF receptor) (p75NTR).
DE (p75 ICD) (low affinity neurotrophin receptor p75NTR).
GN NGFR OR TNFRSF16.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87051725; PubMed=3022937;
RA Johnson D., Lathan A., Buck C.R., Sehgal A., Morgan C., Mercer E.,
RA Botwell M., Chao M.;
RT "Expression and structure of the human NGF receptor.";
RL Cell 47:545-554(1986).
RN [2]
RP SEQUENCE OF 1-22 FROM N.A.
RX MEDLINE=89096903; PubMed=2850481;
RA Sehgal A., Patel N., Chao M.;
RT "A constitutive promoter directs expression of the nerve growth factor
RT receptor gene.";
RL Mol. Cell. Biol. 8:3160-3167(1988).
CC -1- FUNCTION: Low affinity receptor which can bind to NGF, BDNF, NT-3,
CC and NT-4. Can mediate cell survival as well as cell death of
CC neural cells.
CC -1- SUBUNIT: Homodimer; disulfide-linked. Interacts with p75NTR-
```

```

CC associated cell death executor.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- PTM: N- AND O-glycosylated.
CC -1- PTM: Phosphorylated on serine residues.
CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC -----
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CC -----
DR EMBL; M14764; AAB59544.1; -.
DR EMBL; M21621; AAA36363.1; -.
DR PIR; A25218; GOHUN.
DR HSSP; P07174; INGR.
DR Genew; HGNC:7809; NGFR.
DR MIM; 162010; -.
DR InterPro; IPR000488; Death.
DR InterPro; IPR01368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR Pfam; PF00531; death; 1.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
DR PROSITE; PS00050; TNFR_NGFR_2; 4.
DR PROSITE; PS00017; DEATH DOMAIN; 1.
KM Receptor; Apoptosis; Neurogenesis; Transmembrane; Glycoprotein;
KT Repeat; Phosphorylation; Signal.
FT CHAIN 29 427
FT SIGNAL 1 28
FT TUMOR NECROSIS FACTOR RECEPTOR
FT SUPERFAMILY MEMBER 16.
FT EXTRACELLULAR (POTENTIAL).
FT POTENTIAL.
FT CYTOPLASMIC (POTENTIAL).
FT TNFR-CYS 1.
FT REPEAT 31 64 TNFR-CYS 2.
FT REPEAT 66 107 TNFR-CYS 3.
FT REPEAT 108 146 TNFR-CYS 4.
FT REPEAT 148 188 TNFR-CYS 4.
FT DOMAIN 344 421 DEATH.
FT DISULFID 197 248 SER/THR-RICH.
FT DISULFID 32 43 BY SIMILARITY.
FT DISULFID 44 57 BY SIMILARITY.
FT DISULFID 47 64 BY SIMILARITY.
FT DISULFID 67 83 BY SIMILARITY.
FT DISULFID 86 99 BY SIMILARITY.
FT DISULFID 89 107 BY SIMILARITY.
FT DISULFID 109 122 BY SIMILARITY.
FT DISULFID 125 138 BY SIMILARITY.
FT DISULFID 128 146 BY SIMILARITY.
FT DISULFID 149 164 BY SIMILARITY.
FT DISULFID 167 180 BY SIMILARITY.
FT DISULFID 170 188 BY SIMILARITY.
FT CARBOHYD 60 60 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 427 AA; 45183 MW; B09FA143FB3D625B CRC64;

Query Match 19.4%; Score 182.5; DB 1; Length 427;
Best Local Similarity 32.1%; Pred. No. 1.6e-08;
Matches 52; Conservative 25; Mismatches 62; Indels 23; Gaps 11;

QY 4 CPQGYIHPONNSICCTCHKGYLYNDCCPGQDTCRECESSGFASSENHLRHCLSC 62
DB 32 CPTGLYTH---SGECCKACNLGEGVAQPC-GANQ-TVCEPCLDSVTSRVASATEPCPK 86
QY 63 SKCREMGQVELSS-CTVDRTVCGCRKNQYRHYSENLFQCFNCSLCLNT-VHLSQD 120
DB 87 TEC---VGLQSSACVCEADAVCRC--AVGYQDETGTGRCACRCVCEAGSLGVSCD 140
QY 121 KQNTVC-TCHAGFFLRE---NECVSCNC---KKSLECK 153
```

Db 141 KONTVCECPDGTYSDEANHVDPCLPCTVCTEDTERQLRECTR 182

RESULT 11

TR16 MOUSE

ID TR16 MOUSE STANDARD; PRT; 417 AA.

AC Q920W1; 37 50 BY SIMILARITY.

DT 15-JUN-2002 (Rel. 41, Created)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Tumor necrosis factor receptor superfamily member 16 precursor (Low-affinity nerve growth factor receptor) (NGF receptor) (Low affinity neurotrophin receptor p75NTR).

DE NGFR OR TNFRSF16.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]_TaxID=10090;

RP SEQUENCE FROM N.A.

RC STRAIN=A;

RX MEDLINE=99077793; PubMed=9857182;

RA Tuffreau C., Benejean J., Blondel D., Kieffer B., Flamand A.;

RT "Low-affinity nerve growth factor receptor (p75NTR) can serve as a receptor for rabies virus.";

RL EMBO J. 17:7250-7259(1998).

CC -!- FUNCTION: Low affinity receptor which can bind to NGF, BDNF, NT-3, and NT-4. Can mediate cell survival as well as cell death of neural cells (By similarity). Binds to rabies virus glycoprotein Gs.

CC -!- SUBUNIT: Homodimer; disulfide-linked. Interacts with p75NTR-associated cell death executor (By similarity).

CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).

CC -!- PTM: N- AND O-glycosylated (By similarity).

CC -!- PTM: Phosphorylated on serine residues (By similarity).

CC -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.

CC -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.

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DR EMBL; AF105292; AAD17943.1; ..

DR HSP; P07174; INGR.

DR MGI; 97323; Ngfr.

DR InterPro; IPR000486; Death.

DR Pfam; PF00531; death; 1.

DR Pfam; PF00020; TNFR_C6; 4.

DR SMART; SM00005; DEATH; 1.

DR SMART; SM00208; TNFR; 3.

DR PROSITE; PS00652; TNFR_NGFR_1; 3.

DR PROSITE; PS00500; TNFR_NGFR_2; 4.

DR PROSITE; PS00017; DEATH_DOMAIN; 1.

DR Receptor; Apoptosis; Neurogenesis; Transmembrane; Glycoprotein; Repeat; Signal.

FT SIGNAL 1 21 BY SIMILARITY.

FT CHAIN 22 417 TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 16.

FT DOMAIN 22 246 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 247 265 POTENTIAL.

FT DOMAIN 266 417 CYTOPLASMIC (POTENTIAL).

FT REPEAT 24 57 TNFR-CYS 1.

FT REPEAT 59 100 TNFR-CYS 2.

FT REPEAT 101 139 TNFR-CYS 3.

FT REPEAT 141 181 TNFR-CYS 4.

FT DOMAIN 190 241 DEATH.

FT DOMAIN 190 241 SER/THR-RICH.

FT DISULFID 25 36 BY SIMILARITY.

FT DISULFID 37 50 BY SIMILARITY.

FT DISULFID 40 57 BY SIMILARITY.

FT DISULFID 60 76 BY SIMILARITY.

FT DISULFID 79 92 BY SIMILARITY.

FT DISULFID 82 100 BY SIMILARITY.

FT DISULFID 102 115 BY SIMILARITY.

FT DISULFID 118 131 BY SIMILARITY.

FT DISULFID 121 139 BY SIMILARITY.

FT DISULFID 142 157 BY SIMILARITY.

FT DISULFID 160 173 BY SIMILARITY.

FT DISULFID 163 181 BY SIMILARITY.

FT CARBOHYD 53 53 N-LINKED (GLCNAC...) (POTENTIAL).

SQ SEQUENCE 417 AA; 44686 MW; 5D7A4510D8AF9B2 CRC64;

Query Match 19.3%; Score 181.5; DB 1; Length 417;

Best Local Similarity 31.5%; Pred. No. 1.9e-08;

Matches 51; Conservative 25; Mismatches 67; Indels 19; Gaps 10;

QY 4 CPOGKIHPQNNISICTCKHGTLYNDGPGQDTPDREC-ESGSFTASENHLRHCLSC 62

DB 25 CSTGMVTH---SGECKACNLGEGVAQPC-GANQ-TVCEPCLDSVTFSVDVSGATEPKPC 79

QY 63 SKCRKEMGQVEISS-CTVDRDVTVCGRKQRYHNSENLFQCFNCSLCLNGT-VHLSQCE 120

DB 80 TEC---LGLQSMAPCVCEADDAVCRC---SYGYQDEETGRCEACSVCGVSGLVFSCOD 133

QY 121 KONTVC-TCHAGFFLRE---NECVSCSNCKSLKCTKCLCP 157

DB 134 KONTVCECPGTYSDEANHVDPCLPCTVCTEDTERQLRECTP 175

RESULT 12

TR16 MOUSE

ID TR16 MOUSE STANDARD; PRT; 474 AA.

AC P25119; P97893;

DT 01-MAY-1992 (Rel. 22, Created)

DT 01-MAY-1992 (Rel. 22, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Tumor necrosis factor receptor superfamily member 1B precursor (Tumor necrosis factor receptor 2) (TNF-R2) (p75).

GN TNFRSF1B OR TNFR2 OR TNFR-2.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]_TaxID=10090;

RP SEQUENCE FROM N.A.

RX MEDLINE=91187885; PubMed=1849278;

RA Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C.,

RA Wong G.H., Chen E.Y., Goeddel D.V.;

RT "Cloning and expression of cDNAs for two distinct murine tumor necrosis factor receptors demonstrate one receptor is species specific.";

RT Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).

RL [2]

RN SEQUENCE FROM N.A.

RP MEDLINE=91246168; PubMed=1645445;

RX Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I.,

RA Copeland N.G., Jenkins N.A., Smith C.A.;

RT "Molecular cloning and expression of the type 1 and type 2 murine receptors for tumor necrosis factor.";

RT Mol. Cell. Biol. 11:3020-3026(1991).

RL [3]

RN SEQUENCE OF 1-26 FROM N.A.

RP STRAIN=NOD;

RC JACOB C.O., LIU J.;

RA Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.

RN [4]

RP TISSUE=Liver;

RC Kisonerghis M., Fellows R., Feldmann M., Chernajovsky Y.;

RA Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: Receptor with high affinity for TNFSF2/TNF-alpha and

approximately 5-fold lower affinity for homotrimeric TNF α /lymphotxin- α (By similarity).

CC SUBCELLULAR LOCATION: Type I membrane protein.

CC - SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.

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DR EMBL: M60469; AAA39752.1; -

DR EMBL: M59378; AAA40463.1; -

DR EMBL: U39488; AAA65021.1; -

DR EMBL: X87128; CAA60618.1; -

DR PIR: B38634; B38634.

DR HSSP: P19438; INCF.

DR MGI: MGI:1314883; Tnf α sflb.

DR InterPro: IPR001368; TNFR_c6.

DR Pfam: PF00020; TNFR_c6; 4.

DR ProDom: PD000771; TNFR_c6; 1.

DR SMART: SM00208; TNFR; 4.

DR PROSITE: PS00652; TNFR_NGFR_1; 2.

DR PROSITE: PS50050; TNFR_NGFR_2; 3.

DR KEGG: Receptor; Transmembrane; Glycoprotein; Repeat; Signal.

FT SIGNAL 1 22

FT CHAIN 23 474

FT DOMAIN 23 258 TUMOR NECROSIS FACTOR RECEPTOR

FT TRANSMEM 259 288 SUPERFAMILY MEMBER 1B.

FT DOMAIN 289 474 EXTRACELLULAR (POTENTIAL).

FT REPEAT 39 77 POTENTIAL.

FT REPEAT 78 119 CYTOPLASMIC (POTENTIAL).

FT REPEAT 120 164 TNFR-CYS 1.

FT REPEAT 165 203 TNFR-CYS 2.

FT DISULFID 40 54 TNFR-CYS 3.

FT DISULFID 55 68 TNFR-CYS 4.

FT DISULFID 58 76 BY SIMILARITY.

FT DISULFID 79 94 BY SIMILARITY.

FT DISULFID 97 111 BY SIMILARITY.

FT DISULFID 101 119 BY SIMILARITY.

FT DISULFID 121 127 BY SIMILARITY.

FT DISULFID 136 145 BY SIMILARITY.

FT DISULFID 139 163 BY SIMILARITY.

FT DISULFID 166 181 BY SIMILARITY.

FT CARBOHYD 69 69 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT SEQUENCE 474 AA; 50319 MW; 462EAE398C4D6563 CRC64;

Query Match 19.2%; Score 181; DB 1; Length 474;

Best Local Similarity 31.7%; Pred. No. 2.3e-08;

Matches 51; Conservative 20; Mismatches 76; Indels 14; Gaps 8;

QY 4 CPOGKYTHPNNISICTCKHKTLYLVNDCPGPDTCRECESSGFASNNHLHCISC- 62

DB 40 CQISEYVDRAKQWCMCAKCPGQYVYKFC-NKTSPTVACADEASMYQVWVQFTCLSCS 98

QY 63 SKCREKMOVLESCTVADTVYCGCRKQY----RHVSENLPFCFNCSLCLNG-TVHLS 117

DB 99 SSSCTTD--QVEIRACTCKQONVCACEAGRYCALKTH--SSGCRQOMRLSKGPGFVASS 154

QY 118 COEKONTVC-TCHAGFLRENECVSCSNCKSLSECTKCLP 157

DB 155 RAPNGNVLCACAPGTF--SDTSTSDVCRPHRISILAIP 193

RESULT 13

ID VT2 MYXVL STANDARD; PRT; 326 AA.

AC P29825;

DT 01-APR-1993 (Rel. 25, Created)

01-APR-1993 (Rel. 25, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Tumor necrosis factor soluble receptor precursor (Protein T2).

GN M002L OR T2.

OS Myxoma virus (strain Lausanne).

CC Viruses; dsDNA viruses, no RNA stage; Chordopoxvirinae;

CC Leporipoxvirus.

OX NCBI_Taxid=31530;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE=9135768; PubMed=1651597;

RT Upon C., Macen J.L., Schreiber M., McFadden G.;

RT "Myxoma virus expresses a secreted protein with homology to the tumor necrosis factor receptor gene family that contributes to viral virulence."

RT Virology 184:370-382 (1991).

RN [2]

RP SEQUENCE FROM N.A.

RA MEDLINE=20032073; PubMed=10562494;

RA Cameron C., Hota-Mitchell S., Chen L., Barrett J., Cao J.X., Macaulay C., Miller D., Evans D., McFadden G.;

RT "The complete DNA sequence of myxoma virus."

RT Virology 264:298-318 (1999).

CC - FUNCTION: BINDS TO TNF- α AND THEREBY DEAMPENING THE POTENTIAL REACH CELLULAR TARGET AND THEREBY PREVENTS TNF TO ANTIVIRAL EFFECTS OF THE CYTOKINE.

CC - SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.

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DR EMBL: M95181; AAA46632.1; -

DR EMBL: AF1070726; AAP15046.1; -

DR EMBL: AF1070726; AAP14887.1; -

DR EMBL: A23729; CAA01688.1; -

DR PIR: A40566; GOVZML.

DR HSSP: P19438; INCF.

DR InterPro: IPR001368; TNFR_c6.

DR Pfam: PF00020; TNFR_c6; 2.

DR ProDom: PD000771; TNFR_c6; 1.

DR SMART: SM00208; TNFR; 3.

DR PROSITE: PS00652; TNFR_NGFR_1; 2.

DR PROSITE: PS50050; TNFR_NGFR_2; 2.

DR KEGG: Receptor; Glycoprotein; Repeat; Signal.

FT SIGNAL 1 16

FT CHAIN 17 326

FT REPEAT 27 62 TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR.

FT REPEAT 63 104 TNFR-CYS 1.

FT REPEAT 105 147 TNFR-CYS 2.

FT REPEAT 148 186 TNFR-CYS 3.

FT DISULFID 28 39 TNFR-CYS 4.

FT DISULFID 40 53 BY SIMILARITY.

FT DISULFID 43 61 BY SIMILARITY.

FT DISULFID 64 79 BY SIMILARITY.

FT DISULFID 82 96 BY SIMILARITY.

FT DISULFID 86 104 BY SIMILARITY.

FT DISULFID 106 120 BY SIMILARITY.

FT DISULFID 123 146 BY SIMILARITY.

FT DISULFID 129 149 BY SIMILARITY.

FT DISULFID 144 185 BY SIMILARITY.

FT CARBOHYD 66 66 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 181 181 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 205 205 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 228 238 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT SEQUENCE 326 AA; 35208 MW; ABBF027B947292FF CRC64;

Query Match 19.1%; Score 179.5; DB 1; Length 326;

Best Local Similarity 27.4%; Pred. No. 2.3e-08;

```

FT REPEAT      27   62          TNFR-CYS 1.
FT REPEAT      63   104         TNFR-CYS 2.
FT REPEAT     105   147         TNFR-CYS 3.
FT REPEAT     148   186         TNFR-CYS 4.
FT DISULFID    28   39           BY SIMILARITY.
FT DISULFID    40   53           BY SIMILARITY.
FT DISULFID    43   61           BY SIMILARITY.
FT DISULFID    64   79           BY SIMILARITY.
FT DISULFID    82   96           BY SIMILARITY.
FT DISULFID    86  104           BY SIMILARITY.
FT DISULFID   106  120           BY SIMILARITY.
FT DISULFID   123  146           BY SIMILARITY.
FT DISULFID   129  149           BY SIMILARITY.
FT DISULFID   164  185           BY SIMILARITY.
FT CARBOHYD    105  105           N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD   181  181           N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD   205  205           N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD   238  238           N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE    325 AA; 35132 MW; 810530339198A71E CRC64;

Query Match              18.9%; Score 178; DB 1; Length 325;
Best Local Similarity    29.8%; Pred.No.3e-08;
Matches 45; Conservative 15; Mismatches 62; Indels 30; Gaps 6;

QY 13 QNNSICCTCKHGTYLYNDPCGQCQDTDCRECSGSFTAENHLRHCLSC-SKCRKEMGQ 71
       : : : : | | | | : | | | | | | | | | | | | | | | | | | |
Db 34 EKDLCCASCHPGFYASRLC-GFGSNTVSCPCEGTFTASTNHAPACVSCRGPCTGHLS- 91
       : : : : | | | | : | | | | | | | | | | | | | | | | | | |

QY 72 VEISSCTVDRTVGGRKNQRYHWSENLFQCFNCSLCLNGTVHLSQEQEKONTVCTCHAG 131
       : : : : | | | | : | | | | | | | | | | | | | | | | | | |
Db 92 -ESQPCDRTHDRVCMSTGNYYCLKKGQN-----GCRICAPQT-----KC PAG 132

QY 132 FFLRENECVSCSNKK-----SLECTKLC 155
       : : : : | | | | : | | | | | | | | | | | | | | | | | | |
Db 133 YGVSGHTRAGDTLCKERCPHPHTYSDLSPTERC 164

RESULT 15
TNR6 PIG
ID TNR6_PIG STANDARD; PRT; 332 AA.
AC Q7736;
AT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 6 precursor (FASL
DE receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen)
DE (CD95).
GN TNFRSF6 OR APT1 OR FAS.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Buthera; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxId=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Bartling B., Hoffmann J., Holtz J., Schulz R., Heusch G., Darmer D.;
RT "Expression of apoptosis-associated genes in hibernating and stunned
RL myocardium of pig.";
RL Submitted (JAN-1998) to the ENBL/GenBank/DBJ databases.
CC -! FUNCTION: Receptor for TNFRSF6/FASL. The adaptor molecule FADD
CC recruits caspase-8 to the activated receptor. The resulting death-
CC inducing signaling complex (DISC) performs caspase-8 proteolytic
CC activation which initiates the subsequent cascade of caspases
CC (aspartate-specific cysteine proteases) mediating apoptosis. FAS-
CC mediated apoptosis may have a role in the induction of peripheral
CC tolerance, in the antigen-stimulated suicide of mature T-cells, or
CC both (by similarity).
CC -! SUBCELLULAR LOCATION: Type I membrane protein.
CC -! DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
CC AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
CC -! SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
CC -! SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 3, 2002, 14:38:48 ; Search time 31 Seconds
(without alignments)
1070.116 Million cell updates/sec

Title: US-09-907-263-2

Perfect score: 941

Sequence: 1 DSVCFQGYIHPQNSICT.....CSNCKSELECKLCLPQIEN 161

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_virus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	780	82.9	446	6 Q95ND3	Q95nd3 felis silve
2	756	80.3	189	6 Q97530	Q97530 canis fami
3	731	77.7	189	6 Q95185	Q95185 felis silve
4	202	21.5	413	11 Q99MM1	Q99mm1 mus musculu
5	193	20.3	387	11 Q9PVD4	Q9pvd4 xenopus lae
6	191	20.3	433	11 Q91ZM6	Q91zm6 rattus norv
7	188	20.0	302	13 Q9PUS0	Q9pus0 salvelinus
8	182.5	19.4	285	13 Q9DGH7	Q9dgh7 gallus gall
9	179.5	19.1	357	13 Q9DF34	Q9df34 brachydanio
10	176.5	18.8	320	12 Q57079	Q57079 cowpox viru
11	176	18.7	459	11 Q62327	Q62327 mus musculu
12	175.5	18.7	312	13 Q9DGH8	Q9dgh8 gallus gall
13	175.5	18.7	322	12 Q72761	Q72761 cowpox viru
14	171.5	18.2	316	12 Q57092	Q57092 ectromelia
15	171.5	18.2	320	12 Q57091	Q57091 ectromelia
16	171.5	18.2	320	12 Q57300	Q57300 ectromelia

ALIGNMENTS

RESULT 1

Q95ND3 PRELIMINARY; PRT; 446 AA.
AC Q95ND3;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Tumor necrosis factor type I.
GN TNFR I.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RA Mizuno T., Goto Y., Baba K., Masuda K., Ohno K., Tsujimoto H.;
RT "Molecular cloning of feline tumor necrosis factor receptor type I
RT (TNFR I) and expression of TNFR I and TNFR II in various disease in
RT cats.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AB051103; BAB55455.1; -.
DR InterPro; IPR000345; CytC_heme_bind.
DR InterPro; IPR000488; Death.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00020; TNFR_c6; 4.
DR SMART; SM00181; EGF_1.
DR PROSITE; PS00190; CYTOCHROME C; UNKNOWN_1.
DR PROSITE; PS0017; DEATH_DOMAIN; 1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_3.
DR PROSITE; PS00500; TNFR_NGFR_2; 3.
SQ SEQUENCE 446 AA; 49563 MW; 217BD331DD8A74AA CRC64;

Query Match 82.9%; Score 780; DB 6; Length 446;
Best Local Similarity 84.1%; Pred. No. 1.5e-78;
Matches 132; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

17 171.5 18.2 482 11 Q88734 mus musculu
18 169 18.0 326 12 Q57120 cowpox viru
19 168 17.9 347 12 Q57119 cowpox viru
20 168 17.9 351 12 Q57121 cowpox viru
21 167.5 17.8 349 12 Q57100 monkeypox v
22 167 17.7 326 12 Q57122 cowpox viru
23 167 17.7 347 12 Q57115 cowpox viru
24 166.5 17.7 349 12 Q57098 camelopox vi
25 166.5 17.7 349 12 Q57111 variola vir
26 166.5 17.7 349 12 Q8UYA7 Q8uyar7 camelopox vi
27 166.5 17.7 349 12 Q89098 Q89098 variola vir
28 166.5 17.7 349 12 Q57284 camelopox vi
29 166 17.6 360 12 Q57118 variola vir
30 165 17.5 277 6 Q8WMQ2 Q8wmq2 ovis aries
31 165 17.5 349 12 Q57109 variola vir
32 164.5 17.5 348 12 Q57103 monkeypox v
33 164.5 17.5 348 12 Q57108 monkeypox v
34 164.5 17.5 348 12 Q57277 monkeypox v
35 164 17.4 348 12 Q57112 variola vir
36 164 17.4 348 12 Q85407 Q85407 variola vir
37 164 17.4 349 12 Q57110 variola vir
38 164 17.4 349 12 Q89118 Q89118 variola vir
39 164 17.4 351 12 Q73559 cowpox viru
40 162.5 17.3 349 12 Q57099 monkeypox v
41 162.5 17.3 349 12 Q57101 monkeypox v
42 162.5 17.3 349 12 Q57102 monkeypox v
43 162.5 17.3 349 12 Q57291 monkeypox v
44 162 17.2 349 12 Q57305 cowpox viru
45 162 17.2 350 12 Q57123 cowpox viru

QY 4 CPOGKYIHPQNNISICCTKCHKGTLYLYNDGPGQDPTDCRECESSGFTASBNHLRHCLSCS 63
 DB 44 CPOGKYIHPQNNISICCTKCHKGTLYLYNDGPGQDPTDCRECESSGFTASBNHLRHCLSCS 103
 QY 64 KCRKEMQVEISSCTVDRTVCGCRKNQRYRYWSENLFOCFNCSLCLNGTVHLSCEKON 123
 DB 104 KCRKEMQVEISSCTVDRTVCGCRKNQRYRYWSENLFOCFNCSLCLNGTVHLSCEKON 163
 QY 124 TVCTCHAGFPLRNECVSCNCKSLCTCLCPOIE 160
 DB 164 TVCTCHAGFPLRNECVSCNCKSLCTCLCPOIE 200

RESULT 2

ID 097530 PRELIMINARY; PRT; 189 AA.
 AC 097530;
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Tumor necrosis factor receptor p60 (Fragment).
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 ON NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRNIN;
 RX MEDLINE=21109092; PubMed=1182158;
 RA Campbell S.E., Nasir L., Argyle D.J., Gault E.A., Duthe S.,
 Bennett D.;
 RT "Cloning of canine IL-1ra, TNFR and TNFR-2";
 RL Vet. Immunol. Immunopathol. 78:207-214(2001).
 DR EMBL; AF013955; AAD01516.1; -.
 DR HSP; P19438; 1NR.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR001368; TNFR_c6.
 DR Pfam; PF00020; TNFR_c6; 3.
 DR SMART; SM00208; TNFR; 3.
 DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
 DR PROSITE; PS00652; TNFR_NGFR_1; 3.
 DR PROSITE; PS50050; TNFR_NGFR_2; 2.
 DR Receptor.
 KW NON_TER
 SQ SEQUENCE 189 AA; 21324 MW; 5D3AD6A5676BF399 CRC64;
 Query Match 80.3%; Score 756; DB 6; Length 189;
 Best Local Similarity 87.0%; Pred. No. 3e-76;
 Matches 127; Conservative 9; Mismatches 10; Indels 0; Gaps 0;
 QY 3 VCPGKYIHPQNNISICCTKCHKGTLYLYNDGPGQDPTDCRECESSGFTASBNHLRHCLSC 62
 DB 43 VCPGKYIHPQNNISICCTKCHKGTLYLYNDGPGQDPTDCRECESSGFTASBNHLRHCLSC 102
 QY 63 SKCRKEMQVEISSCTVDRTVCGCRKNQRYRYWSENLFOCFNCSLCLNGTVHLSCEKON 122
 DB 103 SKCRKEMQVEISSCTVDRTVCGCRKNQRYRYWSENLFOCFNCSLCLNGTVHLSCEKON 162
 QY 123 NTVCTCHAGFPLRNECVSCNCKKS 148
 DB 163 NTVCTCHAGFPLRNECVSCNCKKS 188

RESULT 3

ID 095185 PRELIMINARY; PRT; 189 AA.
 AC 095185;
 DT 01-FEB-1997 (TREMBlrel. 02, Created)
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Tumor necrosis factor receptor p60 (Fragment).
 OS Felis silvestris catus (Cat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 ON NCBI_TaxID=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Duthe S., Nasir L., Eckersall P.D.;
 RT "Felis catus tumour necrosis factor receptor p60 (TNFR-1) mRNA,
 partial cds.";
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U72344; AAB95089.1; -.
 DR HSP; P19438; 1EXT.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR001368; TNFR_c6.
 DR Pfam; PF00020; TNFR_c6; 3.
 DR SMART; SM00208; TNFR; 3.
 DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
 DR PROSITE; PS00652; TNFR_NGFR_1; 3.
 DR PROSITE; PS50050; TNFR_NGFR_2; 3.
 DR Receptor.
 KW NON_TER
 SQ SEQUENCE 189 AA; 21420 MW; F3FBE0CE809D7DBE CRC64;
 Query Match 77.7%; Score 731; DB 6; Length 189;
 Best Local Similarity 85.5%; Pred. No. 1.8e-73;
 Matches 124; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

QY 4 CPOGKYIHPQNNISICCTKCHKGTLYLYNDGPGQDPTDCRECESSGFTASBNHLRHCLSCS 63
 DB 44 CPOGKYIHPQNNISICCTKCHKGTLYLYNDGPGQDPTDCRECESSGFTASBNHLRHCLSCS 103
 QY 64 KCRKEMQVEISSCTVDRTVCGCRKNQRYRYWSENLFOCFNCSLCLNGTVHLSCEKON 123
 DB 104 KCRKEMQVEISSCTVDRTVCGCRKNQRYRYWSENLFOCFNCSLCLNGTVHLSCEKON 163
 QY 124 TVCTCHAGFPLRNECVSCNCKKS 148
 DB 164 TVCTCHAGFPLRNECVSCNCKKS 188

RESULT 4

ID 099MM1 PRELIMINARY; PRT; 413 AA.
 AC 099MM1;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE WSL-1-like protein.
 GN TNFRSF12.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SV.
 RX MEDLINE=21158384; PubMed=11261933;
 RA Wang E.C.Y., Kitson J., Thern A., Williamson J., Farrow S.N.,
 Owen M.J.;
 RT "Genomic structure, expression, and chromosome mapping of the mouse
 homologue for the WSL-1 (DR3, Apo3, TRAMP, LARD, TR3, TNFRSF12)
 gene.";
 RL Immunogenetics 53:59-63(2001).
 DR EMBL; AF329969; AAK11256.1; -.
 DR HSP; P25942; 1CDF.
 DR MGD; MGI:193467; Tnf1sf12.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR001368; TNFR_c6.
 DR Pfam; PF00531; death; 1.
 DR Pfam; PF00020; TNFR_c6; 3.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00208; TNFR; 3.
 DR PROSITE; PS50017; DEATH_DOMAIN; 1.

[illegible]

BL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF296874; AAG02242.1; -
DR HSP; 014763; IDAV.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS50017; DEATH DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
DR NON TER 1
FT 1
SQ SEQUENCE 312 AA; 35275 MW; 5496BCF1E4CE676C CRC64;

Query Match 18.7%; Score 175.5; DB 13; Length 312;
Best Local Similarity 32.7%; Pred. No. 1.6e-11;
Matches 36; Conservative 14; Mismatches 55; Indels 5; Gaps 3;

OY 18 CCTKCHKTYLYNDPCPGODTDCRECSG-SFTASENHLRHCLSCSKCKREMGQV 76
DB 6 CCTKCKRHVKSIDC-EKTOAHCVPRKSGEYMDHINDLDECKRCSCKALGLEVYKN 63
OY 77 CTVDRTVCGCRKNQYRHVSENLFOCFNCSCLNGTVHLSQCKONTVC 126
DB 64 CTSTENACSCAKNHYCN--SSRCEHCSCTVCENGQIEKCTSTDTVC 111

RESULT 13
ID 072761 PRELIMINARY; PRT; 322 AA.
AC 072761

DT 01-AUG-1998 (TRENBLrel. 07, Created)
DT 01-AUG-1998 (TRENBLrel. 07, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE K2R protein.
GN K2R.
OS Cowpox virus (CPV).

OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10243;

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GRI-90;
RX MEDLINE=98229462; PubMed=9568042;
RA Shchelkunov S.N., Safironov P.F., Tolmenin A.V., Petrov N.A.,
RA Ryzankina O.I., Guttorov V.V., Kotwal G.J.;
RT "Species-specific differences in genome organization of cowpox,
RT smallpox, and vaccinia viruses";
RL Virology 243:432-460(1998).

DR EMBL; Y15035; CA75300.1; -
DR HSP; 014763; IDOG.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
SQ SEQUENCE 322 AA; 35412 MW; 774549278D156A9D CRC64;

Query Match 18.7%; Score 175.5; DB 12; Length 322;
Best Local Similarity 27.7%; Pred. No. 1.6e-11;
Matches 41; Conservative 22; Mismatches 60; Indels 25; Gaps 6;

OY 7 GKYTHPONNSICTKCHKTYLYNDPCPGODTDCRECSG-SFTASENHLRHCLSC-SKC 65
DB 33 GTDYNSSNNLCTCKQCPGMWTHSC-NTSNTKCAKCPDPTFTSIINH1PTCLSCGKGC 91
OY 66 RKEMGQVHISCTVDRDTVCGCRKNQYRHVSENLFOCFNCSCLNGTVHLSQCKONTV 125
DB 92 --SSNQVETKSCNTQRECCVCAAGYCEFEFSN-----GRLCVPT----- 132

OY 126 CTGAGFFL--RENECVSCNCKSL 150

DB 133 -KDCSGYGVYSSKGDVICKKCPGNID 159

RESULT 14
ID 057092 PRELIMINARY; PRT; 316 AA.
AC 057092

DT 01-JUN-1998 (TRENBLrel. 06, Created)
DT 01-JUN-1998 (TRENBLrel. 06, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Tumor necrosis factor receptor II homolog.
GN CRMD.
OS Ectromelia virus.

OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=12643;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MUNICH-SF(SILVER FOX);
RX MEDLINE=98188282; PubMed=9520445;
RA Loparev V.N., Parsons J.M., Knight J.C., Panus J.F., Ray C.A.,
RA Buller R.M.L., Pickup D.J., Esposito J.J.;
RT "A third distinct tumor necrosis factor receptor of orthopoxviruses";
RL Proc. Natl. Acad. Sci. U.S.A. 95:3786-3791(1998).
DR EMBL; U87580; AAB94350.1; -
DR HSP; P19438; TEXT.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
KM Receptor.
SQ SEQUENCE 316 AA; 34660 MW; 443CC11B5B4E12A9 CRC64;

Query Match 18.2%; Score 171.5; DB 12; Length 316;
Best Local Similarity 27.8%; Pred. No. 4.4e-11;
Matches 42; Conservative 22; Mismatches 62; Indels 25; Gaps 6;

OY 14 NNSICTKCHKTYLYNDPCPGODTDCRECSG-SFTASENHLRHCLSC-SKCKREMGQV 72
DB 34 SNLCKQCPGMWTHSC-NTSNTKCDKCPDPTFTSIPIHSPACSCRCGK--SSNQV 90
OY 73 EISCTVDRTVCGCRKNQYRHVSENLFOCFNCSCLNGTVHLSQCKONTVCTGAGF 132
DB 91 ETKSSNTQDRVCAAGYCEFEFSN-----GRLCVPT-----KCSGV 132
OY 133 FL--RENECVSCNCKSLCTKCLPQIE 160
DB 133 GYGVYSSKGDVICKKCPGNIDKDLFSNID 163

RESULT 15
ID 057091 PRELIMINARY; PRT; 320 AA.
AC 057091

DT 01-JUN-1998 (TRENBLrel. 06, Created)
DT 01-JUN-1998 (TRENBLrel. 06, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Tumor necrosis factor receptor II homolog.
GN CRMD.
OS Ectromelia virus.

OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=12643;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=MUNICH-MP3;
RX MEDLINE=98188282; PubMed=9520445;
RA Loparev V.N., Parsons J.M., Knight J.C., Panus J.F., Ray C.A.,
RA Buller R.M.L., Pickup D.J., Esposito J.J.;
RT "A third distinct tumor necrosis factor receptor of orthopoxviruses";
RL Proc. Natl. Acad. Sci. U.S.A. 95:3786-3791(1998).
DR EMBL; U87578; AAB94348.1; -

DR HSP; P19438; IEXT.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
KW Receptor.
SQ SEQUENCE 320 AA; 35134 MW; CB0AE80A1F53F5A5 CRC64;

Query Match 18.2%; Score 171.5; DB 12; Length 320;
Best Local Similarity 27.8%; Pred. No. 4.4e-11;
Matches 42; Conservative 22; Mismatches 62; Indels 25; Gaps 6;

Qy 14 NNSICCTKCHGTYLYNDPCPGQDTCRECESGSFTASENHLRLCLSC-SKCRKEMGQV 72
Db 38 SNNLCCQCNPGMYTHSC-NTISNTKDKCPDDTFTSIPNHSAPCLSCRGKC--SSNQV 94

Qy 73 EISSCTVDRDTCVCGCRKNQRYHWSENLFCFNCISLCLNGTVHLSCQEKQNTVCTCHAGF 132
Db 95 ETKSCSNTQDRVCVCASGYCEFEGSN-----GRLCVFQT-----KCGSGY 136

Qy 133 FL---RENECVSCSNCKKSELECTKCLLPQIE 160
Db 137 GYGYSSKGDVICKCPGNIDKCDLSFNSID 167

Search completed: December 3, 2002, 14:41:01
Job time : 33 secs

